



SEQUENCE LISTING

<110> CuraGen Corporation

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<120> Novel Proteins and Nucleic Acids Encoding Same

<130> 15966-750

<140> 09/825,751

<141> 2001-04-03

<150> 60/194,314

<151> 2000-04-03

<150> 60/225,693

<151> 2000-08-16

<160> 85

<170> PatentIn Ver. 2.1

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<211> 1852

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<213> Homo sapiens

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<221> CDS

<222> (208)..(1698)

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tggccctgga ccctgccagc ctggggcttg ggctttgtc cccttgggc cttgagtgtg 180

gccagggttc tggcgattgt gtggta cag aag cca tgt ctg caa cgc ctg cca 234

Gln Lys Pro Cys Leu Gln Arg Leu Pro

tcc gca gac gtg aat gag tgc aat gac cct ggc gtc tgc act aac			282
Ser Ala Asp Val Asn Glu Cys Ala Glu Asn Pro Gly Val Cys Thr Asn			
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Gly Val Cys Val Asn Thr Asp Gly Ser Phe Arg Cys Glu Cys Pro Phe			
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Gly Tyr Ser Leu Asp Phe Thr Gly Ile Asn Cys Val Asp Thr Asp Glu			
45	50	55	
tgc tct gtc ggc cac ccc tgt ggg caa ggg aca tgc acc aat gtc atc			426
Cys Ser Val Gly His Pro Cys Gly Gln Gly Thr Cys Thr Asn Val Ile			
60	65	70	
gga ggc ttc gaa tgt gcc tgt gct gac ggc ttt gag cct ggc ctc atg			474
Gly Gly Phe Glu Cys Ala Cys Ala Asp Gly Phe Glu Pro Gly Leu Met			
75	80	85	
atg acc tgc gag gac atc gac gaa tgc tcc ctg aac ccg ctg ctc tgt			522
Met Thr Cys Glu Asp Ile Asp Glu Cys Ser Leu Asn Pro Leu Leu Cys			
90	95	100	105
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Ala Phe Arg Cys His Asn Thr Glu Gly Ser Tyr Leu Cys Thr Cys Pro			
110	115	120	
gcc ggc tac acc ctg cgg gag gac ggg gcc atg tgt cga gat gtg gac			618
Ala Gly Tyr Thr Leu Arg Glu Asp Gly Ala Met Cys Arg Asp Val Asp			
125	130	135	
gag tgt gca gat ggt cag cag gac tgc cac gcc cgg ggc atg gag tgc			666
Glu Cys Ala Asp Gly Gln Gln Asp Cys His Ala Arg Gly Met Glu Cys			
140	145	150	
aag aac ctc atc ggt acc ttc gcg tgc gtc tgt ccc cca ggc atg cgg			714
Lys Asn Leu Ile Gly Thr Phe Ala Cys Val Cys Pro Pro Gly Met Arg			
155	160	165	
ccc ctg cct ggc tct ggg gag ggc tgc aca gat gac aat gaa tgc cac			762
Pro Leu Pro Gly Ser Gly Glu Gly Cys Thr Asp Asp Asn Glu Cys His			
170	175	180	185
gct cag cct gac ctc tgt gtc aac ggc cgc tgt gtc aac acc gcg ggc			810
Ala Gln Pro Asp Leu Cys Val Asn Gly Arg Cys Val Asn Thr Ala Gly			
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Ser Phe Arg Cys Asp Cys Asp Glu Gly Phe Gln Pro Ser Pro Thr Leu			
205	210	215	
acc gag tgc cac gac atc cgg cag ggg ccc tgc ttt gcc gag gtg ctg			906
Thr Glu Cys His Asp Ile Arg Gln Gly Pro Cys Phe Ala Glu Val Leu			
220	225	230	
cag acc atg tgc cgg tct ctg tcc agc agc agt gag gct gtc acc agg			954
Gln Thr Met Cys Arg Ser Leu Ser Ser Ser Glu Ala Val Thr Arg			
235	240	245	
gcc gag tgc tgc tgt ggg ggt ggc cgg ggc tgg ggg ccc cgc tgc gag			1002
Ala Glu Cys Cys Gly Gly Arg Gly Trp Gly Pro Arg Cys Glu			
250	255	260	265
ctc tgt ccc ctg ccc ggc acc tct gcc tac agg aag ctg tgc ccc cat			1050
Leu Cys Pro Leu Pro Gly Thr Ser Ala Tyr Arg Lys Leu Cys Pro His			
270	275	280	
ggc tca ggc tac act gct gag ggc cga gat gta gat gaa tgc cgt atg			1098
Gly Ser Gly Tyr Thr Ala Glu Gly Arg Asp Val Asp Glu Cys Arg Met			
285	290	295	
ctt gct cac ctg tgt gct cat ggg gag tgc atc aac agc ctt ggc tcc			1146
Leu Ala His Leu Cys Ala His Gly Glu Cys Ile Asn Ser Leu Gly Ser			
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ttc cgc tgc cac tgt cag gcc ggg tac aca ccg gat gct act gct act			1194
Phe Arg Cys His Cys Gln Ala Gly Tyr Thr Pro Asp Ala Thr Ala Thr			
315	320	325	
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Thr Cys Leu Asp Met Asp Glu Cys Ser Gln Val Pro Lys Pro Cys Thr			
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ttc ctc tgc aaa aac acg aag ggc agt ttc ctg tgc agc tgt ccc cga			1290
Phe Leu Cys Lys Asn Thr Lys Gly Ser Phe Leu Cys Ser Cys Pro Arg			
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Gly Tyr Leu Leu Glu Glu Asp Gly Arg Thr Cys Lys Asp Leu Asp Glu			
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Cys Thr Ser Arg Gln His Asn Cys Gln Phe Leu Cys Val Asn Thr Val			
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Gly Gln Gly Thr Cys Thr Asn Val Ile Gly Gly Phe Glu Cys Ala Cys		
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Ala Asp Gly Phe Glu Pro Gly Leu Met Met Thr Cys Glu Asp Ile Asp		
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Glu Cys Ser Leu Asn Pro Leu Leu Cys Ala Phe Arg Cys His Asn Thr		
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Glu Gly Ser Tyr Leu Cys Thr Cys Pro Ala Gly Tyr Thr Leu Arg Glu		
115	120	125
Asp Gly Ala Met Cys Arg Asp Val Asp Glu Cys Ala Asp Gly Gln Gln		
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Asp Cys His Ala Arg Gly Met Glu Cys Lys Asn Leu Ile Gly Thr Phe		
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Ala Cys Val Cys Pro Pro Gly Met Arg Pro Leu Pro Gly Ser Gly Glu		
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Gly Cys Thr Asp Asp Asn Glu Cys His Ala Gln Pro Asp Leu Cys Val		
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Asn Gly Arg Cys Val Asn Thr Ala Gly Ser Phe Arg Cys Asp Cys Asp		
195	200	205
Glu Gly Phe Gln Pro Ser Pro Thr Leu Thr Glu Cys His Asp Ile Arg		
210	215	220
Gln Gly Pro Cys Phe Ala Glu Val Leu Gln Thr Met Cys Arg Ser Leu		
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Ser Ser Ser Ser Glu Ala Val Thr Arg Ala Glu Cys Cys Cys Gly Gly		
245	250	255
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260	265	270
Ser Ala Tyr Arg Lys Leu Cys Pro His Gly Ser Gly Tyr Thr Ala Glu		
275	280	285
Gly Arg Asp Val Asp Glu Cys Arg Met Leu Ala His Leu Cys Ala His		

290

295

300

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325 330 335

Cys Ser Gln Val Pro Lys Pro Cys Thr Phe Leu Cys Lys Asn Thr Lys
340 345 350

Gly Ser Phe Leu Cys Ser Cys Pro Arg Gly Tyr Leu Leu Glu Glu Asp
355 360 365

Gly Arg Thr Cys Lys Asp Leu Asp Glu Cys Thr Ser Arg Gln His Asn
370 375 380

Cys Gln Phe Leu Cys Val Asn Thr Val Gly Ala Phe Thr Cys Arg Cys
385 390 395 400

Pro Pro Gly Phe Thr Gln His His Gln Ala Cys Phe Asp Asn Asp Glu
405 410 415

Cys Ser Ala Gln Pro Gly Pro Cys Gly Ala His Gly His Cys His Asn
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Thr Pro Gly Ser Phe Arg Cys Glu Cys His Gln Gly Phe Thr Leu Val
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Ser Ser Gly His Gly Cys Glu Asp Val Asn Glu Cys Asp Gly Pro His
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<213> Homo sapiens

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tgc

cgg	gcc	ttc	aat	gcg	aag	cct	gct	gcc	acc	atc	atc	tgg	ttc	cgg	96	
Cys	Arg	Ala	Phe	Asn	Ala	Lys	Pro	Ala	Ala	Thr	Ile	Ile	Trp	Phe	Arg	
				20					25						30	

gac

ggg	acg	cag	cag	gag	ggc	gct	gtg	gcc	agc	acg	gaa	ttg	ctg	aag	144	
Asp	Gly	Thr	Gln	Gln	Glu	Gly	Ala	Val	Ala	Ser	Thr	Glu	Leu	Leu	Lys	
				35					40						45	

gat

ggg	aag	agg	gag	acc	acc	gtg	agc	caa	ctg	ctt	att	aac	ccc	acg	192	
Asp	Gly	Lys	Arg	Glu	Thr	Thr	Val	Ser	Gln	Leu	Leu	Ile	Asn	Pro	Thr	
				50					55						60	

gac

ctg	gac	ata	ggg	cgt	gtc	ttc	act	tgc	cga	agc	atg	aac	gaa	gcc	240	
Asp	Leu	Asp	Ile	Gly	Arg	Val	Phe	Thr	Cys	Arg	Ser	Met	Asn	Glu	Ala	
				65					70						80	

atc

cct	agt	ggc	aag	gag	act	tcc	atc	gag	ctg	gat	gtg	cac	cac	cct	288	
Ile	Pro	Ser	Gly	Lys	Glu	Thr	Ser	Ile	Glu	Leu	Asp	Val	His	His	Pro	
				85					90						95	

cct

aca	gtg	acc	ctg	tcc	att	gag	cca	cag	acg	ggg	cag	gag	ggt	gag	336	
Pro	Thr	Val	Thr	Leu	Ser	Ile	Glu	Pro	Gln	Thr	Gly	Gln	Glu	Gly	Glu	
				100					105						110	

cgt

gtt	gtc	ttt	acc	tgc	cag	gcc	aca	gcc	aac	ccc	gag	atc	t	379		
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Cys

Arg	Ala	Phe	Asn	Ala	Lys	Pro	Ala	Ala	Thr	Ile	Ile	Trp	Phe	Arg	
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20	25	30
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35	40	45
Asp Gly Lys Arg Glu Thr Thr Val Ser Gln Leu Leu Ile Asn Pro Thr		
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Asp Leu Asp Ile Gly Arg Val Phe Thr Cys Arg Ser Met Asn Glu Ala		
65	70	75
Ile Pro Ser Gly Lys Glu Thr Ser Ile Glu Leu Asp Val His His Pro		
85	90	95
Pro Thr Val Thr Leu Ser Ile Glu Pro Gln Thr Gly Gln Glu Gly Glu		
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		15	
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Cys Pro Val Gly His Arg Leu Ser Asp Ser Ser Ala Ala Cys Glu Asp			
20	25	30	
tac cgg gcc ggc gcc tgc ttc tca gtg ctt ttc ggg ggc cgc tgt gct			143
Tyr Arg Ala Gly Ala Cys Phe Ser Val Leu Phe Gly Gly Arg Cys Ala			
35	40	45	
gga gac ctc gcc ggc cac tac act cgc agg cag tgc tgc tgt gac agg			191
Gly Asp Leu Ala Gly His Tyr Thr Arg Arg Gln Cys Cys Cys Asp Arg			
50	55	60	

ggc agg tgc tgg gca gct ggc ccg gtc cct gag ctg tgt cct cct cgg			239
Gly Arg Cys Trp Ala Ala Gly Pro Val Pro Glu Leu Cys Pro Pro Arg			
65	70	75	
ggc tcc aat gaa ttc cag caa ctg tgc gcc cag cgg ctg cct ctt cta			287
Gly Ser Asn Glu Phe Gln Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu			
80	85	90	95
ccc ggc cac cct ggc ctc ttc cct ggc ctc ctg ggc ttc gga tcc aat			335
Pro Gly His Pro Gly Leu Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn			
100	105	110	
ggc atg ggt ccc cct ctt ggg cca gcg cga ctc aac ccc cat ggc tct			383
Gly Met Gly Pro Pro Leu Gly Pro Ala Arg Leu Asn Pro His Gly Ser			
115	120	125	
gat gcg cgt ggg atc ccc agc ctg ggc cct ggc aac tct aat att ggc			431
Asp Ala Arg Gly Ile Pro Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly			
130	135	140	
act gct acc ctg aac cag acc att gac atc tgc cga cac ttc acc aac			479
Thr Ala Thr Leu Asn Gln Thr Ile Asp Ile Cys Arg His Phe Thr Asn			
145	150	155	
ctg tgt ctg aat ggc cgc tgc ctg ccc acg cct tcc agc tac cgc tgc			527
Leu Cys Leu Asn Gly Arg Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys			
160	165	170	175
gag tgt aac gtg ggc tac acc cag gac gtg cgc ggc gag tgc att gat			575
Glu Cys Asn Val Gly Tyr Thr Gln Asp Val Arg Gly Glu Cys Ile Asp			
180	185	190	
gta gac gaa tgc acc agc agc ccc tgc cac cac ggt gac tgc gtc aac			623
Val Asp Glu Cys Thr Ser Ser Pro Cys His His Gly Asp Cys Val Asn			
195	200	205	
atc ccc ggc acc tac cac tgc cgg tgc tac ccg ggc ttc cag gcc acg			671
Ile Pro Gly Thr Tyr His Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr			
210	215	220	
ccc acc agg cag gca tgc gtg gat gtg gac gag tgc att gtc agt ggt			719
Pro Thr Arg Gln Ala Cys Val Asp Val Asp Glu Cys Ile Val Ser Gly			
225	230	235	
ggc ctt tgt cac ctg ggc cgc tgt gtc aac aca gag ggc agc ttc cag			767
Gly Leu Cys His Leu Gly Arg Cys Val Asn Thr Glu Gly Ser Phe Gln			
240	245	250	255

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tgt ctc aac gag gat ggc agc ttc tcc tgc ctc tgc aaa ccc ggc ttc Cys Leu Asn Glu Asp Gly Ser Phe Ser Cys Leu Cys Lys Pro Gly Phe 290 295 300	911
ctg ctg gcg cct ggc ggc cac tac tgc atg gac att gac gag tgc cag Leu Leu Ala Pro Gly Gly His Tyr Cys Met Asp Ile Asp Glu Cys Gln 305 310 315	959
acg ccc ggc atc tgc gtg aac ggc cac tgt acc aac acc gag ggc tcc Thr Pro Gly Ile Cys Val Asn Gly His Cys Thr Asn Thr Glu Gly Ser 320 325 330 335	1007
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tgt cct gcc aaa aac tcc gct gag ttc cag gca ctg tgc agc agt ggg Cys Pro Ala Lys Asn Ser Ala Glu Phe Gln Ala Leu Cys Ser Ser Gly 400 405 410 415	1247
ctt ggc att acc acg gat ggt cga gac atc aac gag tgt gct ctg gat Leu Gly Ile Thr Thr Asp Gly Arg Asp Ile Asn Glu Cys Ala Leu Asp 420 425 430	1295
cct gag gtt tgt gcc aat ggc gtg tgc gag aac ctt cgg ggc agc tac Pro Glu Val Cys Ala Asn Gly Val Cys Glu Asn Leu Arg Gly Ser Tyr 435 440 445	1343

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Arg Cys Val Cys Asn Leu Gly Tyr Glu Ala Gly Ala Ser Gly Lys Asp		
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tgc aca gac gtg gat gag tgt gcc ctc aac agc ctc ctg tgt gac aac		1439
Cys Thr Asp Val Asp Glu Cys Ala Leu Asn Ser Leu Leu Cys Asp Asn		
465	470	475
ggg tgg tgc cag aat agc cct ggc agc tac agc tgc tcc tgc ccc ccc		1487
Gly Trp Cys Gln Asn Ser Pro Gly Ser Tyr Ser Cys Ser Cys Pro Pro		
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495		
ggc ttc cac ttc tgg cag gac acg gag atc tgc aaa gat gtc gac gaa		1535
Gly Phe His Phe Trp Gln Asp Thr Glu Ile Cys Lys Asp Val Asp Glu		
500	505	510
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Cys Leu Ser Ser Pro Cys Val Ser Gly Val Cys Arg Asn Leu Ala Gly		
515	520	525
tcc tac acc tgc aaa tgt ggc cct ggc agc cgg ctg gac ccc tct ggt		1631
Ser Tyr Thr Cys Lys Cys Gly Pro Gly Ser Arg Leu Asp Pro Ser Gly		
530	535	540
acc ttc tgt cta gac agc acc aag ggc acc tgc tgg ctg aag atc cag		1679
Thr Phe Cys Leu Asp Ser Thr Lys Gly Thr Cys Trp Leu Lys Ile Gln		
545	550	555
gag agc cgc tgt gag gtg aac ctt cag gga gcc agc ctg cgg tct gag		1727
Glu Ser Arg Cys Glu Val Asn Leu Gln Gly Ala Ser Leu Arg Ser Glu		
560	565	570
575		
tgc tgt gcc acc ctc ggg gca gcc tgg ggg agc ccc tgc gaa cgc tgc		1775
Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly Ser Pro Cys Glu Arg Cys		
580	585	590
gag atc gac cct gcc tgt gcc cgg ggc ttt gcc cgg atg acg ggt gtc		1823
Glu Ile Asp Pro Ala Cys Ala Arg Gly Phe Ala Arg Met Thr Gly Val		
595	600	605
acc tgc gat gat gtg aac gag tgt gag tcc ttc ccg gga gtc tgt ccc		1871
Thr Cys Asp Asp Val Asn Glu Cys Ser Phe Pro Gly Val Cys Pro		
610	615	620
aac ggg cgt tgc gtc aac act gct ggg tct ttc cgc tgt gag tgt cca		1919
Asn Gly Arg Cys Val Asn Thr Ala Gly Ser Phe Arg Cys Glu Cys Pro		
625	630	635

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ctg cct ggc aag tac cgg atg gac gtc tgc tgc tcc atc ggg gcc Leu Pro Gly Lys Tyr Arg Met Asp Val Cys Cys Ser Ile Gly Ala	675	680	685		2063
gtg tgg gga gtc gag tgc gag gcc tgc ccg gat ccc gag tct ctg gag Val Trp Gly Val Glu Cys Glu Ala Cys Pro Asp Pro Glu Ser Leu Glu	690	695	700		2111
ttc gcc agc ctg tgc ccg cgg ggg ctg ggc ttc gcc agc cgg gac ttc Phe Ala Ser Leu Cys Pro Arg Gly Leu Gly Phe Ala Ser Arg Asp Phe	705	710	715		2159
ctg tct ggc cga cca ttc tat aaa gat gtg aat gaa tgc aag gtg ttc Leu Ser Gly Arg Pro Phe Tyr Lys Asp Val Asn Glu Cys Lys Val Phe	720	725	730	735	2207
cct ggc ctc tgc acg cac ggt acc tgc aga aac acg gtg ggc agc ttc Pro Gly Leu Cys Thr His Gly Thr Cys Arg Asn Thr Val Gly Ser Phe	740	745	750		2255
cac tgc gcc tgt gcg ggg ggc ttc gcc ctg gat gcc cag gaa cgg aac His Cys Ala Cys Ala Gly Gly Phe Ala Leu Asp Ala Gln Glu Arg Asn	755	760	765		2303
tgc aca gat atc gac gag tgt cgc atc tct cct gac ctc tgc ggc cag Cys Thr Asp Ile Asp Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Gln	770	775	780		2351
ggc acc tgt gtc aac acg ccg ggc agc ttt gag tgc gag tgt ttt ccc Gly Thr Cys Val Asn Thr Pro Gly Ser Phe Glu Cys Glu Cys Phe Pro	785	790	795		2399
ggc tac gag agt ggc ttc atg ctg atg aag aac tgc atg gac gtg gac Gly Tyr Glu Ser Gly Phe Met Leu Met Lys Asn Cys Met Asp Val Asp	800	805	810	815	2447
gag tgt gca agg gac ccg ctg ctc tgc ccg gga ggc act tgc acc aac Glu Cys Ala Arg Asp Pro Leu Leu Cys Arg Gly Thr Cys Thr Asn	820	825	830		2495

acg gat ggg agc tac aag tgc cag tgt ccc cct ggg cat gag ctg acg			2543
Thr Asp Gly Ser Tyr Lys Cys Gln Cys Pro Pro Gly His Glu Leu Thr			
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gcc aag ggc act gcc tgt gag gac atc gat gag tgc tcc ctg agt gat			2591
Ala Lys Gly Thr Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Ser Asp			
850	855	860	
ggc ctg tgt ccc cat ggc cag tgt gtc aat gtc atc ggt gcc ttc cag			2639
Gly Leu Cys Pro His Gly Gln Cys Val Asn Val Ile Gly Ala Phe Gln			
865	870	875	
tgc tcc tgc cat gcc ggc ttc cag agc aca cct gac cgc cag ggc tgc			2687
Cys Ser Cys His Ala Gly Phe Gln Ser Thr Pro Asp Arg Gln Gly Cys			
880	885	890	895
gtg gac atc aac gaa tgc cgg gtc cag aat ggt ggg tgt gac gtg cac			2735
Val Asp Ile Asn Glu Cys Arg Val Gln Asn Gly Gly Cys Asp Val His			
900	905	910	
cgt att aac act gag ggc agc tac cgg tgc agc tgt ggg cag ggc tac			2783
Arg Ile Asn Thr Glu Gly Ser Tyr Arg Cys Ser Cys Gly Gln Gly Tyr			
915	920	925	
tcg ctg atg ccc gac gga agg gca tgt gca gac gtg gac gag tgt gaa			2831
Ser Leu Met Pro Asp Gly Arg Ala Cys Ala Asp Val Asp Glu Cys Glu			
930	935	940	
gag aac ccc cgc gtt tgt gac caa ggc cac tgc acc aac atg cca ggg			2879
Glu Asn Pro Arg Val Cys Asp Gln Gly His Cys Thr Asn Met Pro Gly			
945	950	955	
ggt cac cgc tgc ctg tgc tat gat ggc ttc atg gcc acg cca gac atg			2927
Gly His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met			
960	965	970	975
agg aca tgt gtt gat gtg gat gag tgt gac ctg aac cct cac atc tgc			2975
Arg Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys			
980	985	990	
ctc cat ggg gac tgc gag aac acg aag ggt tcc ttt gtc tgc cac tgt			3023
Leu His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys			
995	1000	1005	
cag ctg ggc tac atg gtc agg aag ggg gcc aca ggc tgc tct gat gtg			3071
Gln Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val			
1010	1015	1020	

gat gaa tgc gag gtt gga gga cac aac tgt gac agt cac gcc tcc tgt			3119
Asp Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys			
1025	1030	1035	
ctc aac atc ccg ggg agt ttc agc tgt agg tgc ctg cca ggc tgg gtg			3167
Leu Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val			
1040	1045	1050	1055
ggg gat ggc ttc gaa tgt cac gac ctg gat gaa tgc gtc tcc cag gag			3215
Gly Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu			
1060	1065	1070	
cac cgg tgc agc cca aga ggt gac tgt ctc aat gtc cct ggc tcc tac			3263
His Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr			
1075	1080	1085	
cgc tgc acc tgc cgc cag ggc ttt gcc ggg gat ggc ttc ttc tgc gaa			3311
Arg Cys Thr Cys Arg Gln Gly Phe Ala Gly Asp Gly Phe Phe Cys Glu			
1090	1095	1100	
gac agg gat gaa tgt gcc gag aac gtg gac ctc tgt gac aac ggg			3356
Asp Arg Asp Glu Cys Ala Glu Asn Val Asp Leu Cys Asp Asn Gly			
1105	1110	1115	
tagtgccctca atgcgcc			3374

<210> 6

<211> 1118

<212> PRT

<213> Homo sapiens

<400> 6

Gln Gly Gly Ser Cys Val, Asn Met Val Gly Ser Phe His Cys Arg Cys			
1	5	10	15

Pro Val Gly His Arg Leu Ser Asp Ser Ser Ala Ala Cys Glu Asp Tyr			
20	25	30	

Arg Ala Gly Ala Cys Phe Ser Val Leu Phe Gly Gly Arg Cys Ala Gly			
35	40	45	

Asp Leu Ala Gly His Tyr Thr Arg Arg Gln Cys Cys Cys Asp Arg Gly			
50	55	60	

Arg Cys Trp Ala Ala Gly Pro Val Pro Glu Leu Cys Pro Pro Arg Gly			
65	70	75	80

Ser Asn Glu Phe Gln Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu Pro
85 90 95

Gly His Pro Gly Leu Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn Gly
100 105 110

Met Gly Pro Pro Leu Gly Pro Ala Arg Leu Asn Pro His Gly Ser Asp
115 120 125

Ala Arg Gly Ile Pro Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly Thr
130 135 140

Ala Thr Leu Asn Gln Thr Ile Asp Ile Cys Arg His Phe Thr Asn Leu
145 150 155 160

Cys Leu Asn Gly Arg Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys Glu
165 170 175

Cys Asn Val Gly Tyr Thr Gln Asp Val Arg Gly Glu Cys Ile Asp Val
180 185 190

Asp Glu Cys Thr Ser Ser Pro Cys His His Gly Asp Cys Val Asn Ile
195 200 205

Pro Gly Thr Tyr His Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr Pro
210 215 220

Thr Arg Gln Ala Cys Val Asp Val Asp Glu Cys Ile Val Ser Gly Gly
225 230 235 240

Leu Cys His Leu Gly Arg Cys Val Asn Thr Glu Gly Ser Phe Gln Cys
245 250 255

Val Cys Asn Ala Gly Phe Glu Leu Ser Pro Asp Gly Lys Asn Cys Val
260 265 270

Asp His Asn Glu Cys Ala Thr Ser Thr Met Cys Val Asn Gly Val Cys
275 280 285

Leu Asn Glu Asp Gly Ser Phe Ser Cys Leu Cys Lys Pro Gly Phe Leu
290 295 300

Leu Ala Pro Gly Gly His Tyr Cys Met Asp Ile Asp Glu Cys Gln Thr
305 310 315 320

Pro Gly Ile Cys Val Asn Gly His Cys Thr Asn Thr Glu Gly Ser Phe
325 330 335

Arg Cys Gln Cys Leu Gly Gly Leu Ala Val Gly Thr Asp Gly Arg Val
340 345 350

Cys Val Asp Thr His Val Arg Ser Thr Cys Tyr Gly Ala Ile Glu Lys
355 360 365

Gly Ser Cys Ala Arg Pro Phe Pro Gly Thr Val Thr Lys Ser Glu Cys
370 375 380

Cys Cys Ala Asn Pro Asp His Gly Phe Gly Glu Pro Cys Gln Leu Cys
385 390 395 400

Pro Ala Lys Asn Ser Ala Glu Phe Gln Ala Leu Cys Ser Ser Gly Leu
405 410 415

Gly Ile Thr Thr Asp Gly Arg Asp Ile Asn Glu Cys Ala Leu Asp Pro
420 425 430

Glu Val Cys Ala Asn Gly Val Cys Glu Asn Leu Arg Gly Ser Tyr Arg
435 440 445

Cys Val Cys Asn Leu Gly Tyr Glu Ala Gly Ala Ser Gly Lys Asp Cys
450 455 460

Thr Asp Val Asp Glu Cys Ala Leu Asn Ser Leu Leu Cys Asp Asn Gly
465 470 475 480

Trp Cys Gln Asn Ser Pro Gly Ser Tyr Ser Cys Ser Cys Pro Pro Gly
485 490 495

Phe His Phe Trp Gln Asp Thr Glu Ile Cys Lys Asp Val Asp Glu Cys
500 505 510

Leu Ser Ser Pro Cys Val Ser Gly Val Cys Arg Asn Leu Ala Gly Ser
515 520 525

Tyr Thr Cys Lys Cys Gly Pro Gly Ser Arg Leu Asp Pro Ser Gly Thr
530 535 540

Phe Cys Leu Asp Ser Thr Lys Gly Thr Cys Trp Leu Lys Ile Gln Glu
545 550 555 560

Ser Arg Cys Glu Val Asn Leu Gln Gly Ala Ser Leu Arg Ser Glu Cys
565 570 575

Cys Ala Thr Leu Gly Ala Ala Trp Gly Ser Pro Cys Glu Arg Cys Glu
580 585 590

Ile Asp Pro Ala Cys Ala Arg Gly Phe Ala Arg Met Thr Gly Val Thr
595 600 605

Cys Asp Asp Val Asn Glu Cys Glu Ser Phe Pro Gly Val Cys Pro Asn
610 615 620

Gly Arg Cys Val Asn Thr Ala Gly Ser Phe Arg Cys Glu Cys Pro Glu
625 630 635 640

Gly Leu Met Leu Asp Ala Ser Gly Arg Leu Cys Val Asp Val Arg Leu
645 650 655

Glu Pro Cys Phe Leu Arg Trp Asp Glu Asp Glu Cys Gly Val Thr Leu
660 665 670

Pro Gly Lys Tyr Arg Met Asp Val Cys Cys Cys Ser Ile Gly Ala Val
675 680 685

Trp Gly Val Glu Cys Glu Ala Cys Pro Asp Pro Glu Ser Leu Glu Phe
690 695 700

Ala Ser Leu Cys Pro Arg Gly Leu Gly Phe Ala Ser Arg Asp Phe Leu
705 710 715 720

Ser Gly Arg Pro Phe Tyr Lys Asp Val Asn Glu Cys Lys Val Phe Pro
725 730 735

Gly Leu Cys Thr His Gly Thr Cys Arg Asn Thr Val Gly Ser Phe His
740 745 750

Cys Ala Cys Ala Gly Gly Phe Ala Leu Asp Ala Gln Glu Arg Asn Cys
755 760 765

Thr Asp Ile Asp Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Gln Gly
770 775 780

Thr Cys Val Asn Thr Pro Gly Ser Phe Glu Cys Glu Cys Phe Pro Gly
785 790 795 800

Tyr Glu Ser Gly Phe Met Leu Met Lys Asn Cys Met Asp Val Asp Glu
805 810 815

Cys Ala Arg Asp Pro Leu Leu Cys Arg Gly Gly Thr Cys Thr Asn Thr
820 825 830

Asp Gly Ser Tyr Lys Cys Gln Cys Pro Pro Gly His Glu Leu Thr Ala
835 840 845

Lys Gly Thr Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Ser Asp Gly
850 855 860

Leu Cys Pro His Gly Gln Cys Val Asn Val Ile Gly Ala Phe Gln Cys
865 870 875 880

Ser Cys His Ala Gly Phe Gln Ser Thr Pro Asp Arg Gln Gly Cys Val
885 890 895

Asp Ile Asn Glu Cys Arg Val Gln Asn Gly Gly Cys Asp Val His Arg
900 905 910

Ile Asn Thr Glu Gly Ser Tyr Arg Cys Ser Cys Gly Gln Gly Tyr Ser
915 920 925

Leu Met Pro Asp Gly Arg Ala Cys Ala Asp Val Asp Glu Cys Glu Glu
930 935 940

Asn Pro Arg Val Cys Asp Gln Gly His Cys Thr Asn Met Pro Gly Gly
945 950 955 960

His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met Arg
965 970 975

Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys Leu
980 985 990

His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys Gln
995 1000 1005

Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val Asp
1010 1015 1020

Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys Leu
1025 1030 1035 1040

Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val Gly
1045 1050 1055

Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu His
1060 1065 1070

Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr Arg
1075 1080 1085

Cys Thr Cys Arg Gln Gly Phe Ala Gly Asp Gly Phe Phe Cys Glu Asp
1090 1095 1100

Arg Asp Glu Cys Ala Glu Asn Val Asp Leu Cys Asp Asn Gly
1105 1110 1115

<210> 7
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(292)

<400> 7
t cac ggg aat aag cct ggg ccc gtc cct ttg att tcc aac aag atc tgc 49
His Gly Asn Lys Pro Gly Pro Val Pro Leu Ile Ser Asn Lys Ile Cys
1 5 10 15

aac cac agg gac gtg tac ggt ggc atc atc tcc ccc tcc atg ctc tgc 97
Asn His Arg Asp Val Tyr Gly Ile Ile Ser Pro Ser Met Leu Cys
20 25 30

gcg ggc tac ctg acg ggt ggc gtg gac agc tgc cag ggg gac agc ggg 145
Ala Gly Tyr Leu Thr Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
35 40 45

ggg ccc ctg gtg tgt caa gag agg agg ctg tgg aag tta gtg gga gcg 193
Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala
50 55 60

acc agc ttt ggc atc ggc tgc gca gag gtg aac aag cct ggg gtg tac 241
Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr
65 70 75 80

acc gtg tca cct cct tcc tgg act gga tcc acg agc aga tgg aga gag 289
Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu
85 90 95

acc taaaaacctg aagaggaagg ggataagtag ccacctgagt tcctgaggtg 342
Thr

atgaagacag cccgatcctc ccctggactc ccgtgttagga acctgcacac gagcagacac 402
ccttggagct ctgagttccg gcaccagtag caggccc 439

<210> 8

<211> 97
<212> PRT
<213> Homo sapiens

<400> 8

His	Gly	Asn	Lys	Pro	Gly	Pro	Val	Pro	Leu	Ile	Ser	Asn	Lys	Ile	Cys
1				5				10						15	

Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu Cys

	20			25			30								
--	----	--	--	----	--	--	----	--	--	--	--	--	--	--	--

Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly

	35			40			45								
--	----	--	--	----	--	--	----	--	--	--	--	--	--	--	--

Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala

	50			55			60								
--	----	--	--	----	--	--	----	--	--	--	--	--	--	--	--

Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr

	65			70			75					80			
--	----	--	--	----	--	--	----	--	--	--	--	----	--	--	--

Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu

	85			90			95								
--	----	--	--	----	--	--	----	--	--	--	--	--	--	--	--

Thr

<210> 9
<211> 410
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(410)

<400> 9

tg	tca	ttg	tcc	ttt	tac	cta	tta	tat	ttt	ttc	ata	ctc	tgt	gaa	aac	47
Ser	Leu	Ser	Phe	Tyr	Leu	Leu	Tyr	Phe	Phe	Ile	Leu	Cys	Glu	Asn		
1				5					10					15		

aaa tca gtt gcc gga cta acc atg acc tat gat gga aat aat cca gtg 95

Lys	Ser	Val	Ala	Gly	Leu	Thr	Met	Thr	Tyr	Asp	Gly	Asn	Asn	Pro	Val	
					20			25						30		

aca tct cat aga gat gtg cca ctt tct tat tgc aac tca gac tgc aat 143

Thr	Ser	His	Arg	Asp	Val	Pro	Leu	Ser	Tyr	Cys	Asn	Ser	Asp	Cys	Asn	

35	40	45	
tgt gat gaa agt cag tgg gaa cca gtc tgt ggg aac aat gga ata act 191			
Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr			
50	55	60	
tac ctg tca cct tgt cta gca gga tgc aaa tcc tca agt ggt att aaa 239			
Tyr Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys			
65	70	75	
aag cat aca gtg ttt tat aac tgt agt tgt gtg gaa gta act ggt ctc 287			
Lys His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu			
80	85	90	95
cag aac aga aat tac tca gcg cac ttg ggt gaa tgc cca aga gat aat 335			
Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn			
100	105	110	
act tgt aca agg aaa ttt ttc atc tat gtt gca att caa gtc ata aac 383			
Thr Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn			
115	120	125	
tct ttg ttc tct gca aca gga ggt acc 410			
Ser Leu Phe Ser Ala Thr Gly Gly Thr			
130	135		
<210> 10			
<211> 136			
<212> PRT			
<213> Homo sapiens			
<400> 10			
Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn Lys			
1	5	10	15
Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val Thr			
20	25	30	
Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn Cys			
35	40	45	
Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr Tyr			
50	55	60	
Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys Lys			
65	70	75	80

His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu Gln
85 90 95

Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn Thr
100 105 110

Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn Ser
115 120 125

Leu Phe Ser Ala Thr Gly Gly Thr
130 135

<210> 11

<211> 322

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(320)

<400> 11

tg gca gcc ctg gag gag ccg atg gtg gac ctg gac ggc gag ctg cct 47
Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
1 5 10 15

ttc gtg cgg ccc ctg ccc cac att gcc gtg ctc cag gac gag ctg ccg 95
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
20 25 30

caa ctc ttc cag gat gac gac gtc ggg gcc gat gag gaa gag gca gag 143
Gln Leu Phe Gln Asp Asp Val Gly Ala Asp Glu Glu Ala Glu
35 40 45

ttg cgg ggc gaa cac acg ctc aca gag aag ttt gtc tgc ctg gat gac 191
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
50 55 60

tcc ttt ggc cat gac tgc agc ttg acc tgt gat gac tgc agg aac gga 239
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
65 70 75

ggg acc tgc ctc ctg ggc ctg gat ggc tgt gat tgc ccc gag ggg tgg 287
Gly Thr Cys Leu Leu Gly Leu Asp Gly Cys Asp Cys Pro Glu Gly Trp
80 85 90 95

act ggg gtt att tgc aat gag att tgt cct ccg ga
Thr Gly Val Ile Cys Asn Glu Ile Cys Pro Pro
100 105

<210> 12
<211> 106
<212> PRT
<213> Homo sapiens

<400> 12
Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro Phe
1 5 10 15

Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro Gln
20 25 30

Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu Leu
35 40 45

Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp Ser
50 55 60

Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly Gly
65 70 75 80

Thr Cys Leu Leu Gly Leu Asp Gly Cys Asp Cys Pro Glu Gly Trp Thr
85 90 95

Gly Val Ile Cys Asn Glu Ile Cys Pro Pro
100 105

<210> 13
<211> 1332
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(1306)

<400> 13
c gcc ttc atg ctg ccg gcg ggc tgc tcg cgc cgg ctg gtg gcc gag ctg 49
Ala Phe Met Leu Pro Ala Gly Cys Ser Arg Arg Leu Val Ala Glu Leu
1 5 10 15

cag	ggc	gcc	ctg	gac	gcc	tgc	gca	cag	cga	caa	ttg	caa	ttg	gag	cag		97	
Gln	Gly	Ala	Leu	Asp	Ala	Cys	Ala	Gln	Arg	Gln	Leu	Gln	Leu	Glu	Gln			
20								25						30				
agc	ctg	cgc	gtt	tgc	cgt	cgg	ctg	cat	gcc	tgg	gaa	cca	act	ggg		145		
Ser	Leu	Arg	Val	Cys	Arg	Arg	Leu	Leu	His	Ala	Trp	Glu	Pro	Thr	Gly			
35								40					45					
acc	cg	gct	ttg	aag	cca	cct	cca	ggg	cca	gaa	act	aat	gga	gag	gac		193	
Thr	Arg	Ala	Leu	Lys	Pro	Pro	Gly	Pro	Glu	Thr	Asn	Gly	Glu	Asp				
50					55					60								
ccc	ctt	cca	gca	tgc	aca	ccc	agt	cca	caa	gac	ctc	aaa	gag	ttg	gag		241	
Pro	Leu	Pro	Ala	Cys	Thr	Pro	Ser	Pro	Gln	Asp	Leu	Lys	Glu	Leu	Glu			
65					70					75				80				
ttt	ctg	acc	cag	gca	ctg	gag	aag	gct	gta	cga	gtt	cga	aga	ggc	atc		289	
Phe	Leu	Thr	Gln	Ala	Leu	Glu	Lys	Ala	Val	Arg	Val	Arg	Arg	Gly	Ile			
85						90					95							
act	aag	gcc	gaa	gag	aga	gac	aag	gcc	ccc	agc	ctg	aaa	tct	agg	tcc		337	
Thr	Lys	Ala	Glu	Glu	Arg	Asp	Lys	Ala	Pro	Ser	Leu	Lys	Ser	Arg	Ser			
100						105					110							
att	gtc	acc	tct	tct	ggc	acg	aca	gcc	tcc	gcc	cca	ccg	cat	tcc	cca		385	
Ile	Val	Thr	Ser	Ser	Gly	Thr	Thr	Ala	Ser	Ala	Pro	Pro	His	Ser	Pro			
115						120					125							
ggc	caa	gct	ggt	ggc	cat	gct	tca	gac	acg	aga	ccc	acc	aag	ggc	ctc		433	
Gly	Gln	Ala	Gly	Gly	His	Ala	Ser	Asp	Thr	Arg	Pro	Thr	Lys	Gly	Leu			
130						135					140							
cgc	cag	acc	acg	gtg	cct	gcc	aag	ggc	cac	cct	gag	cgc	cg	ctg	ctg		481	
Arg	Gln	Thr	Thr	Val	Pro	Ala	Lys	Gly	His	Pro	Glu	Arg	Arg	Leu	Leu			
145					150					155				160				
tca	gtg	ggg	gat	ggg	acc	cgt	gtt	ggg	atg	gga	gcc	cga	acc	ccc	agg		529	
Ser	Val	Gly	Asp	Gly	Thr	Arg	Val	Gly	Met	Gly	Ala	Arg	Thr	Pro	Arg			
165						170					175							
cct	ggg	g	gc	gc	ctc	agg	gac	cag	caa	atg	gcc	cca	tcc	gct	gct	cct		577
Pro	Gly	Ala	Gly	Leu	Arg	Asp	Gln	Gln	Met	Ala	Pro	Ser	Ala	Ala	Pro			
180						185					190							
cag	gcc	cca	gaa	gcc	ttc	aca	ctc	aag	gag	aag	ggg	cac	ctg	ctg	cg		625	
Gln	Ala	Pro	Glu	Ala	Phe	Thr	Leu	Lys	Glu	Lys	Gly	His	Leu	Leu	Arg			
195						200					205							

ctg cct gca ttc agg aaa gca gct tcc cag aac tcg agc ctg tgg		673
Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp		
210	215	220
gcc cag ctc agt tcc aca cag acc agt gat tcc acg gat gcc gcc gct		721
Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala		
225	230	235
240		
gcc aaa acc cag ttc ctc cag aac atg cag aca gct tca ggc ggg ccc		769
Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro		
245	250	255
cag ccc agg ctc agt gct gtg gag gtg gag gcg gag ggc ggg cgc ctg		817
Gln Pro Arg Leu Ser Ala Val Glu Val Ala Glu Ala Gly Arg Leu		
260	265	270
cgg aag gcc tgc tcg ctg aga ctg cgc atg agg gag gag ctc tca		865
Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser		
275	280	285
gca gcc ccc atg gac tgg atg cag gag tac cgc tgc ctg ctc acg ctg		913
Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu		
290	295	300
gag ggg ctg cag gcc atg gtg ggc cag tgt ctg cac agg ctg cag gag		961
Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu		
305	310	315
320		
ctg cgt gca gcg gtg gcg gaa cag cca cca aga cca tgt cct gtg ggg		1009
Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly		
325	330	335
agg ccc ccc gga gcc tcg ccg tcc tgt ggg ggt aga gcg gag cct gca		1057
Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala		
340	345	350
tgg agc ccc cag ctg ctt gtc tac tcc agc acc cag gag ctg cag acc		1105
Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr		
355	360	365
ctg gcg gcc ctc aag ctg cga gtg gct gtg ctg gac cag cag atc cac		1153
Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His		
370	375	380
ttg gaa aag gtc ctg atg gct gaa ctc ctc ccc ctg gta agc gct gca		1201
Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala		
385	390	395
400		

cag ccg cag ggg ccg ccc tgg ctg gcc ctg tgc cg^g gct gtg cac agc 1249
Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser
405 410 415

ctg ctc tgc gag gga gga gca cgt gtc ctt acc atc ctg cg^g gat gaa 1297
Leu Leu Cys Glu Gly Ala Arg Val Leu Thr Ile Leu Arg Asp Glu
420 425 430

cct gca gtc tgaggccttc ccatgctgcc ctccgc 1332
Pro Ala Val
435

<210> 14

<211> 435

<212> PRT

<213> Homo sapiens

<400> 14

Ala Phe Met Leu Pro Ala Gly Cys Ser Arg Arg Leu Val Ala Glu Leu
1 5 10 15

Gln Gly Ala Leu Asp Ala Cys Ala Gln Arg Gln Leu Gln Leu Glu Gln
20 25 30

Ser Leu Arg Val Cys Arg Arg Leu Leu His Ala Trp Glu Pro Thr Gly
35 40 45

Thr Arg Ala Leu Lys Pro Pro Pro Gly Pro Glu Thr Asn Gly Glu Asp
50 55 60

Pro Leu Pro Ala Cys Thr Pro Ser Pro Gln Asp Leu Lys Glu Leu Glu
65 70 75 80

Phe Leu Thr Gln Ala Leu Glu Lys Ala Val Arg Val Arg Arg Gly Ile
85 90 95

Thr Lys Ala Glu Glu Arg Asp Lys Ala Pro Ser Leu Lys Ser Arg Ser
100 105 110

Ile Val Thr Ser Ser Gly Thr Thr Ala Ser Ala Pro Pro His Ser Pro
115 120 125

Gly Gln Ala Gly Gly His Ala Ser Asp Thr Arg Pro Thr Lys Gly Leu
130 135 140

Arg Gln Thr Thr Val Pro Ala Lys Gly His Pro Glu Arg Arg Leu Leu
145 150 155 160

Ser Val Gly Asp Gly Thr Arg Val Gly Met Gly Ala Arg Thr Pro Arg
165 . 170 . 175

Pro Gly Ala Gly Leu Arg Asp Gln Gln Met Ala Pro Ser Ala Ala Pro
180 185 190

Gln Ala Pro Glu Ala Phe Thr Leu Lys Glu Lys Gly His Leu Leu Arg
195 200 205

Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp
210 215 220

Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala
225 230 235 240

Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro
245 250 255

Gln Pro Arg Leu Ser Ala Val Glu Val Glu Ala Glu Ala Gly Arg Leu
260 265 270

Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser
275 280 285

Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu
290 295 300

Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu
305 310 315 320

Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly
325 330 335

Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala
340 345 350

Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr
355 360 365

Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His
370 375 380

Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala
385 390 395 400

Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser
405 410 415

Leu Leu Cys Glu Gly Gly Ala Arg Val Leu Thr Ile Leu Arg Asp Glu
420 425 430

Pro Ala Val
435

<210> 15
<211> 513
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(510)

<400> 15
atg cag gct caa cag tac cag cag cgt cga aaa ttt gca gct gcc 48
Met Gln Ala Gln Gln Tyr Gln Gln Arg Arg Lys Phe Ala Ala Ala
1 5 10 15

ttc ttg gca ttc att ttc ata ctg gca gct gtg gat act gct gaa gca 96
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
20 25 30

ggg aag aaa gag aaa cca gaa aaa aaa gtg aag aag tct gac tgt gga 144
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly
35 40 45

gaa tgg cag tgg agt gtg tgt gtg ccc acc agt gga gac tgt ggg ctg 192
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu
50 55 60

ggc aca cgg gag ggc act cgg act gga gct gag tgc aag caa acc atg 240
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
65 70 75 80

aag acc cag aga tgt aag atc ccc tgc aac tgg aag aag caa ttt ggc 288
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
85 90 95

gcg gag tgc aaa tac cag ttc cag gcc tgg gga gaa tgt gac ctg aac 336
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
100 105 110

aca gcc ctg aag acc aga act gga agt ctg aag cga gcc ctg cac aat 384

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn				
115	120	125		
gcc gaa tgc cag aag act gtc acc atc tcc aag ccc tgt ggc aaa ctg	432			
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu				
130	135	140		
acc aag ccc aaa cct caa ggt acc cta gaa ctt aaa gta aaa aaa aaa	480			
Thr Lys Pro Lys Pro Gln Gly Thr Leu Glu Leu Lys Val Lys Lys Lys				
145	150	155	160	
aaa aaa aaa aaa aat tct gag gag acc ttt tag	513			
Lys Lys Lys Asn Ser Glu Glu Thr Phe				
165	170			
<210> 16				
<211> 170				
<212> PRT				
<213> Homo sapiens				
<400> 16				
Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala				
1	5	10	15	
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala				
20	25	30		
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly				
35	40	45		
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu				
50	55	60		
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met				
65	70	75	80	
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly				
85	90	95		
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn				
100	105	110		
Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn				
115	120	125		
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu				
130	135	140		

Thr Lys Pro Lys Pro Gln Gly Thr Leu Glu Leu Lys Val Lys Lys Lys
145 150 155 160

Lys Lys Lys Asn Ser Glu Glu Thr Phe
165 170

<210> 17
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (16)..(297)

<400> 17
cgaagggctt tcaca atg cta ggt gtg gtc tgg ctg gtg gca gtc atc gta 51
Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
1 5 10

gga tca ccc atg tgg cac gtg caa caa ctt gag atc aaa tat gac ttc 99
Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
15 20 25

cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg acc agc cct 147
Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Trp Thr Ser Pro
30 35 40

gtg cac cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctc 195
Val His Gln Lys Ile Tyr Thr Phe Ile Leu Val Ile Leu Phe Leu
45 50 55 60

ctg cct ctt atg gaa gaa acg agc tgt cat tat gat ggt gac agt 243
Leu Pro Leu Met Glu Glu Thr Ser Cys His Tyr Asp Gly Asp Ser
65 70 75

ggt ggc tct ctt tgc tgt gtg ctg ggc acc att cca tgt tgt cca tat 291
Gly Gly Ser Leu Cys Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr
80 85 90

gat gat tgaatacagt aattttgaaa aggaatatga tggatgtcaca atcaagatga 347
Asp Asp

tttttgctat cgtgcaaatt attggatttt ccaactccat ctgtaatccc attgtctatg 407

catttatgaa tgaaaacttc aaaaa

432

<210> 18

<211> 94

<212> PRT

<213> Homo sapiens

<400> 18

Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val Gly Ser Pro Met
1 5 10 15

Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe Leu Tyr Glu Lys
20 25 30

Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro Val His Gln Lys
35 40 45

Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu Leu Pro Leu Met
50 55 60

Glu Glu Glu Thr Ser Cys His Tyr Asp Gly Asp Ser Gly Gly Ser Leu
65 70 75 80

Cys Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr Asp Asp
85 90

<210> 19

<211> 1425

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (31)..(1395)

<400> 19

ctcctgggga gacgcagcca cttgcccgcc atg gat act ccc agg gtc ctg ctc 54
Met Asp Thr Pro Arg Val Leu Leu
1 5

tcg gcc gtc ttc ctc atc agt ttt ctg tgg gat ttg ccc ggt ttc cag 102
Ser Ala Val Phe Leu Ile Ser Phe Leu Trp Asp Leu Pro Gly Phe Gln
10 15 20

cag gct tcc atc tca tcc tcc tgt tcg tcc gcc gag ctg ggt tcc acc 150

Gln	Ala	Ser	Ile	Ser	Ser	Cys	Ser	Ser	Ala	Glu	Leu	Gly	Ser	Thr			
25				30					35				40				
aag	ggc	atg	cga	agc	cgc	aag	gaa	ggc	aag	atg	cag	cgg	gcg	ccg	cgc	198	
Lys	Gly	Met	Arg	Ser	Arg	Lys	Glu	Gly	Lys	Met	Gln	Arg	Ala	Pro	Arg		
						45				50				55			
gac	agt	gac	gac	ggc	cgg	gag	ggc	cag	gaa	cca	cag	ccg	cgg	cct	cag	246	
Asp	Ser	Asp	Asp	Ala	Gly	Arg	Glu	Gly	Gln	Glu	Pro	Gln	Pro	Arg	Pro	Gln	
						60				65				70			
gac	gaa	ccc	cgg	gct	cag	cag	ccc	cgg	gcg	cag	gag	ccg	cca	ggc	agg	294	
Asp	Glu	Pro	Arg	Ala	Gln	Gln	Pro	Arg	Ala	Gln	Glu	Pro	Pro	Gly	Arg		
						75				80				85			
ggt	ccg	cgc	gtg	gtg	ccc	cac	gag	tac	atg	ctg	tca	atc	tac	agg	act	342	
Gly	Pro	Arg	Val	Val	Pro	His	Glu	Tyr	Met	Leu	Ser	Ile	Tyr	Arg	Thr		
						90				95				100			
tac	tcc	atc	gct	gag	aag	ctg	ggc	atc	aat	gcc	agc	ttt	ttc	cag	tct	390	
Tyr	Ser	Ile	Ala	Glu	Lys	Leu	Gly	Ile	Asn	Ala	Ser	Phe	Phe	Gln	Ser		
						105				110				115		120	
tcc	aag	tcg	gct	aat	acg	atc	acc	agc	ttt	gta	gac	agg	gga	cta	gac	438	
Ser	Lys	Ser	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Val	Asp	Arg	Gly	Leu	Asp		
						125				130				135			
gat	ctc	tcg	cac	act	cct	ctc	cgg	aga	cag	aag	tat	ttg	ttt	gat	gtg	486	
Asp	Leu	Ser	His	Thr	Pro	Leu	Arg	Arg	Gln	Lys	Tyr	Leu	Phe	Asp	Val		
						140				145				150			
tcc	atg	ctc	tca	gac	aaa	gaa	gag	ctg	gtg	ggc	gcg	gag	ctg	cgg	ctc	534	
Ser	Met	Leu	Ser	Asp	Lys	Glu	Glu	Leu	Val	Gly	Ala	Glu	Leu	Arg	Leu		
						155				160				165			
ttt	cgc	cag	gcf	ccc	tca	gcf	ccc	tgg	ggg	cca	cca	gcc	ggg	ccg	ctc	582	
Phe	Arg	Gln	Ala	Pro	Ser	Ala	Pro	Trp	Gly	Pro	Pro	Ala	Gly	Pro	Leu		
						170				175				180			
cac	gtg	cag	ctc	tcc	cct	tgc	ttt	tcg	ccc	cta	ctg	ctg	gac	gcf	cgg	630	
His	Val	Gln	Leu	Phe	Pro	Cys	Leu	Ser	Pro	Leu	Leu	Leu	Asp	Ala	Arg		
						185				190				195		200	
acc	ctg	gac	ccg	cag	ggg	gcf	ccg	ccg	gcc	ggc	tgg	gaa	gtc	ttc	gac	678	
Thr	Leu	Asp	Pro	Gln	Gly	Ala	Pro	Pro	Ala	Gly	Trp	Glu	Val	Phe	Asp		
						205				210				215			
gtg	tgg	cag	ggc	ctg	cgc	cac	cag	ccc	tgg	aag	cag	ctg	tgc	ttg	gag	726	

Val Trp Gln Gly Leu Arg His Gln Pro Trp Lys Gln Leu Cys Leu Glu			
220	225	230	
ctg cgg gcc gca tgg ggc gag ctg gac gcc ggg gag gcc gag gcg cgc			774
Leu Arg Ala Ala Trp Gly Glu Leu Asp Ala Gly Glu Ala Glu Ala Arg			
235	240	245	
gcg cgg gga ccc cag caa ccg ccc ccg gac ctg cgg agt ctg ggc			822
Ala Arg Gly Pro Gln Gln Pro Pro Pro Asp Leu Arg Ser Leu Gly			
250	255	260	
ttc ggc cgg agg gtg cgg cct ccc cag gag cgg gcc ctg ctg gtg gta			870
Phe Gly Arg Arg Val Arg Pro Pro Gln Glu Arg Ala Leu Leu Val Val			
265	270	275	280
ttc acc aga tcc cag cgc aag aac ctg ttc gca gag atg cgc gag cag			918
Phe Thr Arg Ser Gln Arg Lys Asn Leu Phe Ala Glu Met Arg Glu Gln			
285	290	295	
ctg ggc tcg gcc gag gct gcg ggc ccg ggc gcg ggc gcc gag ggg tcg			966
Leu Gly Ser Ala Glu Ala Ala Gly Pro Gly Ala Gly Ala Glu Gly Ser			
300	305	310	
tgg ccg ccg tcg ggc gcc ccg gat gcc agg cct tgg ctg ccc tcg			1014
Trp Pro Pro Pro Ser Gly Ala Pro Asp Ala Arg Pro Trp Leu Pro Ser			
315	320	325	
ccc ggc cgc cgg cgg cgc acg gcc ttc gcc agt cgc cat ggc aag			1062
Pro Gly Arg Arg Arg Arg Thr Ala Phe Ala Ser Arg His Gly Lys			
330	335	340	
cgg cac ggc aag aag tcc agg cta cgc tgc agc aag aag ccc ctg cac			1110
Arg His Gly Lys Lys Ser Arg Leu Arg Cys Ser Lys Lys Pro Leu His			
345	350	355	360
gtg aac ttc aag gag ctg ggc tgg gac gac tgg att atc gcg ccc ctg			1158
Val Asn Phe Lys Glu Leu Gly Trp Asp Asp Trp Ile Ile Ala Pro Leu			
365	370	375	
gag tac gag gcc tat cac tgc gag ggt gta tgc gac ttc ccg ctg cgc			1206
Glu Tyr Glu Ala Tyr His Cys Glu Gly Val Cys Asp Phe Pro Leu Arg			
380	385	390	
tcg cac ctg gag ccc acc aac cac gcc atc atc cag acg ctg atg aac			1254
Ser His Leu Glu Pro Thr Asn His Ala Ile Ile Gln Thr Leu Met Asn			
395	400	405	
tcc atg gac ccc ggc tcc acc ccg ccc agc tgc tgc gtg ccc acc aaa			1302

Ser	Met	Asp	Pro	Gly	Ser	Thr	Pro	Pro	Ser	Cys	Cys	Val	Pro	Thr	Lys	
410					415							420				
ttg act ccc atc agc att cta tac atc gac gcg ggc aat aat gtg gtc															1350	
Leu	Thr	Pro	Ile	Ser	Ile	Leu	Tyr	Ile	Asp	Ala	Gly	Asn	Asn	Val	Val	
425					430							435			440	
tac	aag	cag	tac	gag	gac	atg	gtg	gtg	gag	tcg	tgc	ggc	tgc	agg		1395
Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	Val	Glu	Ser	Cys	Gly	Cys	Arg		
						445				450			455			
tagcggtgcc tttcccgccg ccttggcccg															1425	
<210> 20																
<211> 455																
<212> PRT																
<213> Homo sapiens																
<400> 20																
Met	Asp	Thr	Pro	Arg	Val	Leu	Leu	Ser	Ala	Val	Phe	Leu	Ile	Ser	Phe	
1					5					10				15		
Leu	Trp	Asp	Leu	Pro	Gly	Phe	Gln	Gln	Ala	Ser	Ile	Ser	Ser	Ser	Cys	
					20					25				30		
Ser	Ser	Ala	Glu	Leu	Gly	Ser	Thr	Lys	Gly	Met	Arg	Ser	Arg	Lys	Glu	
						35				40				45		
Gly	Lys	Met	Gln	Arg	Ala	Pro	Arg	Asp	Ser	Asp	Ala	Gly	Arg	Glu	Gly	
						50				55				60		
Gln	Glu	Pro	Gln	Pro	Arg	Pro	Gln	Asp	Glu	Pro	Arg	Ala	Gln	Gln	Pro	
						65				70				75		80
Arg	Ala	Gln	Glu	Pro	Pro	Gly	Arg	Gly	Pro	Arg	Val	Val	Pro	His	Glu	
						85				90				95		
Tyr	Met	Leu	Ser	Ile	Tyr	Arg	Thr	Tyr	Ser	Ile	Ala	Glu	Lys	Leu	Gly	
						100				105				110		
Ile	Asn	Ala	Ser	Phe	Phe	Gln	Ser	Ser	Lys	Ser	Ala	Asn	Thr	Ile	Thr	
						115				120				125		
Ser	Phe	Val	Asp	Arg	Gly	Leu	Asp	Asp	Leu	Ser	His	Thr	Pro	Leu	Arg	
						130				135				140		
Arg	Gln	Lys	Tyr	Leu	Phe	Asp	Val	Ser	Met	Leu	Ser	Asp	Lys	Glu	Glu	

145	150	155	160
Leu Val Gly Ala Glu Leu Arg Leu Phe Arg Gln Ala Pro Ser Ala Pro			
165	170	175	
Trp Gly Pro Pro Ala Gly Pro Leu His Val Gln Leu Phe Pro Cys Leu			
180	185	190	
Ser Pro Leu Leu Leu Asp Ala Arg Thr Leu Asp Pro Gln Gly Ala Pro			
195	200	205	
Pro Ala Gly Trp Glu Val Phe Asp Val Trp Gln Gly Leu Arg His Gln			
210	215	220	
Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala Ala Trp Gly Glu Leu			
225	230	235	240
Asp Ala Gly Glu Ala Glu Ala Arg Ala Arg Gly Pro Gln Gln Pro Pro			
245	250	255	
Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly Arg Arg Val Arg Pro Pro			
260	265	270	
Gln Glu Arg Ala Leu Leu Val Val Phe Thr Arg Ser Gln Arg Lys Asn			
275	280	285	
Leu Phe Ala Glu Met Arg Glu Gln Leu Gly Ser Ala Glu Ala Ala Gly			
290	295	300	
Pro Gly Ala Gly Ala Glu Gly Ser Trp Pro Pro Pro Ser Gly Ala Pro			
305	310	315	320
Asp Ala Arg Pro Trp Leu Pro Ser Pro Gly Arg Arg Arg Arg Arg Thr			
325	330	335	
Ala Phe Ala Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu			
340	345	350	
Arg Cys Ser Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp			
355	360	365	
Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu			
370	375	380	
Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His			
385	390	395	400
Ala Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro			

405

410

415

Pro Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr
420 425 430

Ile Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
435 440 445

Val Glu Ser Cys Gly Cys Arg
450 455

<210> 21

<211> 1852

<212> DNA

<213> Homo sapiens

<400> 21

cgatgactc ccgagaaggt gagccctca cccacatgt aagagcccct tctgggccac 60
ccagatccat ctccgcactg cctgggtctc tggtttcag gtcctccctg agagcctggg 120
tggccctgga ccctgccagc ctggggcttg ggctttgtc cccttggggc cttgagtgtg 180
gccagggtctc tggcattgt gtggtacag aagccatgtc tgcaacgcct gccatccgca 240
gacgtgaatg agtgtgcaga gaaccctggc gtctgcacta acggcgctcg tgtcaacacc 300
gatggatcct tccgtgtga gtgtccctt ggctacagcc tggacttcac tggcatcaac 360
tgtgtggaca cagacgagtg ctctgtcggc cacccctgtg ggcaaggggac atgcaccaat 420
gtcatcgag gcttcaatg tgcctgtgt gacggctttg agcctggcct catgatgacc 480
tgcgaggaca tcgacgaatg ctccctgaac ccgtcgctct gtgccttccg ctgccacaat 540
accgagggtctc cctacctgtg cacctgtcca gcccgtaca ccctgccccgaa ggacggggcc 600
atgtgtcgag atgtggacga gtgtcagat ggtcagcagg actgccacgc cccccggcatg 660
gagtgcaga acctcatcg taccttcgcg tgcgtctgtc ccccaaggcat gcggccctg 720
cctggctctg gggagggctg cacagatgac aatgaatgcc acgctcagcc tgacctctgt 780
gtcaacggcc gctgtgtcaa cacccggc agcttccggc gcgactgtga tgagggattc 840
cagcccagcc ccacccctac cgagtgcac gacatccggc agggccctg cttgccgag 900
gtgctgcaga ccatgtgcgg gtctctgtcc agcagcagtg aggctgtcac cagggccgag 960
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gttagatgaat gccgtatgct tgctcacctg tgtgtcatg gggagtgcatacagcctt 1140
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aagggcaggta tcctgtgcag ctgtccctca ggctacactgc tggaggagga tggcaggacc 1320
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aacaccccccgg gcagcttccg ctgtgaatgc caccaaggct tcaccctggt cagctcaggc 1560
catggctgtg aagatgtgaa tgaatgtgat gggcccccacc gctgccagca tggctgtcag 1620
aaccagctag gggctaccg ctgcagctgc ccccaagggtt tcacccagca ctcccaatgg 1680
gcccagtg tgggtgagtg aaaagggtg ggaagaagct gggccctcca ccagaatctg 1740

ctcagagcag gcgactaaca gacgccaccc tgcaagatga tgtgacaagg acaatttatct 1800
aaagattgaa cagggcagcc cagaagatga gaatgagtgt gccctgtcgc cc 1852

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:For Ag 390
primer

<400> 22
accaatgtca tcggaggctt 20

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rev Ag 390
primer

<400> 23
gatgtcctcg caggtcatca t 21

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ag390
primer

<400> 24
tcaaagccgt cagcacaggc aca 23

<210> 25
<211> 379
<212> DNA
<213> Homo sapiens

<400> 25
ggaggggcctg tgattctact gcaggcaggc accccccaca acctcacatg cccgggccttc 60
aatgcgaagc ctgctgccac catcatctgg ttccgggacg ggacgcagca ggagggcgct 120
gtggccagca cgaaattgct gaaggatggg aagagggaga ccaccgtgag ccaactgctt 180
attaaccca cggacctgga catagggcgt gtcttcaactt gccgaagcat gaacgaagcc 240
atcccctagtg gcaaggagac ttccatcgag ctggatgtgc accaccctcc tacagtgacc 300
ctgtccatgt agccacagac ggggcaggag ggtgagcgtg ttgtctttac ctgccaggcc 360
acagccaaacc ccgagatct 379

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 271
primer

<400> 26
acctggacat agggcgtgtc t 21

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Ag 271
primer

<400> 27
tcgatggaag tctccttgcc 20

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ag 271
primer

<400> 28
cgaagcatga acgaagccat cccttag 26

<210> 29
<211> 234
<212> DNA
<213> Homo sapiens

<400> 29
tccaaatctca catgcacgca cagccggcct gaggcggtcca gcatcaggcc ctctggacac 60
tcacagcgga aagacccagc agtgttgcg caacgcccgt tgggacagac tcccgaaa 120
gactcacact cgttcacatc atcgcggtg acacccgtca tccgggaaa gccccgggca 180
caggcagggc cgatctcgca gcgttcgcag gggctcccc aggctgcccc gagg 234

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 72
primer

<400> 30
cgaaaaagacc cagcagtgtt 20

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Ag 72
primer

<400> 31
atgatgtgaa cgagtgtgag tcctt 25

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ag 72
primer

<400> 32
cgcccgttgg gacagactcc c 21

<210> 33
<211> 439
<212> DNA
<213> Homo sapiens

<400> 33
tcacggaaat aagcctgggc ccgtcccttt gattccaac aagatctgca accacaggga 60
cgtgtacgtt ggcatcatct cccccctccat gctctgcgcg ggctacctga cgggtggcgt 120
ggacagctgc cagggggaca gcggggggcc cctggtgtgt caagagagga ggctgtggaa 180
gttagtggga ggcaccagct ttggcatcgg ctgcgcagag gtgaacaagc ctgggtgtta 240
caccgtgtca cctccttcct ggactggatc cacgagcaga tggagagaga cctaaaaacc 300
tgaagagggaa gggataagt agccaccta gttcctgagg tcatgaagac agcccgatcc 360
tcccctggac tcccgtgttag gaacctgcac acgagcagac acccttggag ctctgagttc 420
cgccaccagt agcaggccc 439

<210> 34
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 248
primer

<400> 34
tttccaacaa gatctgcaac ca 22

<210> 35
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Ag 248
primer

<400> 35
aggtagcccg cgcaagag 17

<210> 36
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ag 248
primer

<400> 36
cgtgtacggt ggcatcatct cccc

24

<210> 37
<211> 410
<212> DNA
<213> Homo sapiens

<400> 37
tgtcattgtc ctttaccta ttatatttt tcatactctg tgaaaacaaa tcagttgccg 60
gactaaccat gacctatgtat ggaaataatc cagtgacatc tcatagagat gtgccacttt 120
cttattgcaa ctcagactgc aattgtatgt aaagtcaatc ggaaccatgc tggggaaaca 180
atgaaataac ttacctgtca ctttgtctag cagatgcaa atccctcaatc ggtttaaaa 240
agcatacagt gtttataac tgttagttgt tgaaatgtac tggctccatc aacagaaatt 300
actcagcgca cttgggtgaa tgcccaagag ataatacttg tacaaggaaa ttttcatct 360
atgttgcata tcaagtata aactctttgt tctctgcac aggaggtacc 410

<210> 38
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 287
primer

<400> 38
aactcagact gcaattgtga tgaaa

25

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Ag 287
primer

<400> 39
ctagacaagg tgacaggtaa gttattcc 28

<210> 40
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ag 287
primer

<400> 40
ttgttcccac agactggttc ccactgt 27

<210> 41
<211> 322
<212> DNA
<213> Homo sapiens

<400> 41
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tgccccacat tgccgtgctc caggacgagc tgccgcaact cttccaggat gacgacgtcg 120
ggcccgatga ggaagaggca gagttgcggg gcgaacacac gctcacagag aagtttgtct 180
gcctggatga ctcccttggc catgactgca gcttgacctg tgatgactgc aggaacggag 240
ggacctgcct cctgggcctg gatggctgtg attgccccga ggggtggact ggggttattt 300
gcaatgagat ttgtcctccg ga 322

<210> 42
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 252
primer

<400> 42
gagctgccgc aactcttcc 19

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Ag 252
primer

<400> 43
gacaaaacttc tctgtgagcg tgtg

24

<210> 44
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ag 252
primer

<400> 44
cgcaactctg cctttcctc atcgg

25

<210> 45
<211> 1332
<212> DNA
<213> Homo sapiens

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ggacgcctgc gcacagcgac aattgcaatt ggagcagagc ctgcgcgtt gccgtcggt 120
gctgcatgcc tgggaaccaa ctgggacccg ggcttgaag ccacctccag ggccagaaac 180
taatggagag gaccgccttc cagcatgcac acccagtcca caagacctca aagagttgga 240
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agagagagac aaggccccca gcctgaaatc tagtccatt gtcacctttt ctggcacgac 360
agcctccgcc ccaccgcatt ccccaggcca agctggtggc catgcttcag acacgagacc 420
caccaagggc ctccgcccaga ccacggtgc tgccaagggc caccctgagc gccggctgct 480
gtcagtgggg gatgggaccc gtgttggat gggagccga acccccaggc ctggggcggg 540
cctcagggac cagcaaatgg ccccatccgc tgctcctcag gccccagaag cttcacact 600
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gctgccctcg gc 1332

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ab16
Primer

<400> 46
ggcattcagg aaagcagctt 20

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Ab16
Primer

<400> 47
gcatccgtgg aatcactgg 20

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ab16
Primer

<400> 48
tgggcccagc tcagttccac aca 23

<210> 49
<211> 513
<212> DNA
<213> Homo sapiens

<400> 49
atgcaggctc aacagtacca gcagcagcgt cgaaaatttgcagctgcctt cttggcattc 60
attttcatac tggcagctgt ggatactgct gaagcaggaa agaaaagagaa accagaaaaaa 120
aaagtgaaga agtctgactg tggagaatgg cagtggagtg tgtgtgtgcc caccagtgg 180
gactgtggc tggcacacg ggagggcact cgactggag ctgagtgcaa gcaaaccatg 240
aagacccaga gatgttaagat cccctgcaac tggagaagc aatttggcgc ggagtgc当地 300
taccagttcc aggctgggg agaatgtgac ctgaacacag ccctgaagac cagaactgg 360
agtctgaagc gagcctgca caatgccaa tgccagaaga ctgtcaccat ctccaagccc 420
tgtggcaaac tgaccaagcc caaacctcaa ggtaccctag aacttaaagt aaaaaaaaaa 480
aaaaaaaaaaa aaaattctga ggagaccttt tag 513

<210> 50
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 177
Primer

<400> 50
ccctgcacaa tgccaat 18

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 177
Primer

<400> 51
tgaggtttgg gcttggtcag 20

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 177
Primer

<400> 52
caccatctcc aagccctgtg gcaa 24

<210> 53
<211> 432
<212> DNA
<213> Homo sapiens

<400> 53
ttttgaagt tttcattcat aaatgcata gcaatggat tacagatgga gttggaaaat 60
ccaataattt gcacgatagc aaaaatcatc ttgattgtga catcatcata ttcctttca 120
aaattactgt attcaatcat catatggaca acatggaatg gtgcccagca cacagcaaag 180
agagccacca ctgtcaccat cataatgaca gctcgttct tcttccataa gaggcaggag 240
gaagaggatg acaaggatga aggtggtgta gatcttctgg tgcacagggc tggccactc 300
ttctaagcag cagatgtgtt cctttcata taggaagtca tatttgatct caagttgtt 360
cacgtgccac atgggtgatc ctacgatgac tgccaccagc cagaccacac cttagcattgt 420
gaaagccctt cg 432

<210> 54
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward GPCR 13
Primer

<400> 54
atggaatggc gcccagca 18

<210> 55
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse GPCR
13 Primer

<400> 55
tggaaagaaga aacgagctgt ca 22

<210> 56
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe GPCR 13
Primer

<400> 56

cagcaaagag agccaccact gtcacca

27

<210> 57
<211> 102
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(2)
<223> Wherein n is a or t or g or c.

<220>
<221> misc_feature
<222> (101)..(102)
<223> Wherein n is t or a or g or c.

<400> 57
nngacttact ccatcgctga gaagctggc atcaatgcc a gcttttcca gtcttccaag 60
tcggctaata cgatcaccag ctgttagac agggactag nn 102

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Ag 191
Primer

<400> 58
gacttactcc atcgctgaga agct

24

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Ag 191
Primer

<400> 59
gctggtgatc gtattagccg a

21

<210> 60
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Ag 191
Primer

<400> 60
catcaatgcc agcttttcc agtcttcc

28

<210> 61
<211> 238
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (104)
<223> Wherein n is t or a or g or c.

<400> 61
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gagtccggtg tgtggacact gacgagtgct ccatcgccaa cccntgcggg aacgggacat 120
gcaccaacgt gatcggtgc ttcaatgca cctgcaacga aggcttgag ccggggccca 180
tgatgaactg cgaagacatc aacgagtgta cccagaaccc gctgctctgt gcttccg 238

<210> 62
<211> 197
<212> DNA
<213> Mus musculus

<400> 62
aagccatgca acttcatctg caagaacacc aaggcagtt accagtgctc ctgcccacgg 60
gggtacgtcc tgcaggagga cggaaaagacg tgcaaagacc tcgacgaatg tcaaaccaaa 120
cagcacaact gccagttct ctgtgtcaac accctgggg gattcacctg taaatgtccg 180

<210> 63

<211> 492

<212> PRT

<213> Homo sapiens

<400> 63

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Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val															
															30
20 25															
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro															
															45
35 40															
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val															
															60
50															
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys															
															80
65 70 75															
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val															
															95
85 90															
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys															
															110
100 105															
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn															
															125
115 120															
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp															
															140
130 135															
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met															
															160
145 150 155															
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp															
															175
165 170															
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn															
															190
180 185															
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser															
															205
195 200															

Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
210 215 220

Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225 230 235 240

Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
245 250 255

Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
260 265 270

Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
275 280 285

Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
290 295 300

Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305 310 315 320

Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
325 330 335

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
340 345 350

Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
355 360 365

Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
370 375 380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385 390 395 400

Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
405 410 415

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
420 425 430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
435 440 445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
450 455 460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465 470 475 480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asp Gly
485 490

<210> 64

<211> 2656

<212> DNA

<213> Homo sapiens

<400> 64

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<210> 65

<211> 1011

<212> PRT

<213> Drosophila melanogaster

<400> 65

Met Ala Leu Arg Gln Ser Ala Lys Asp Val Ala Lys Ser Asn Cys Val
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20 25 30

Ala Leu Val Asp Ser Ser Thr Ala Gln Val Asp Thr Thr Ile Ser Gln
35 40 45

Gln Glu Ser Gln Ser Val Val Leu Pro Cys Pro Val Asp Ala Glu Lys
50 55 60

Cys Gly Lys Leu His Ser Leu Asn Trp Phe Lys Gly Asp Asp Arg Ile
65 70 75 80

Ala Ala Met Leu Leu Gly Asp Ser Asn Val Thr Ser Val Asn Lys Glu
85 90 95

Phe Asp Glu Arg Val Thr Val Glu Gln Asn Pro Tyr Arg Leu Val Ile
100 105 110

Lys Asp Leu Lys Ile Ala Asp Glu Asp Ile Tyr Leu Cys Asp Thr Thr
115 120 125

Phe Phe Ile Pro Glu Glu Thr Cys Asp Asn Phe Asn Gly Tyr Arg Ile
130 135 140

Glu Leu Arg Val Leu Val Pro Pro Thr Glu Val Val Ile Leu Asp Ala
145 150 155 160

Lys Gly Asp Arg Ile Lys Asn Gly Ser Val Val Gly Pro Met Gln Glu
165 170 175

Arg Gln Ser Leu Lys Ala Thr Cys Thr Val Arg Asn Thr Arg Pro Gln
180 185 190

Pro Glu Val Ser Trp Phe Arg Gly Thr Lys Arg Leu Thr Thr Tyr Ser
195 200 205

Pro Thr His Asp Leu Val Asp Gly Leu Tyr Thr Ser Thr Leu Glu Leu
210 215 220

Asp Trp Thr Leu Ser Arg Glu Asp Leu Ala Gln Asp Ile Glu Cys Arg
225 230 235 240

Val Lys Ser Ala Ala Ile Gln Asn Val Thr Val Thr Lys Phe Ser Val
245 250 255

Asp Leu Gln Val Arg Pro Thr Ser Ile Asp Ile Asn Gly Val Lys His
260 265 270

His Thr Val Gln Gly Ser Lys Val Val Leu Thr Cys Asp Ile His Gly
275 280 285

Ala Arg Pro Ala Val Asn Leu Thr Trp Tyr Asn Thr Thr Thr Ile Ile
290 295 300

Ser Ser Gly Glu Asn Glu Ile Thr Glu Val Arg Ser Lys Ser Leu Glu
305 310 315 320

Lys Ser Asp Gly Thr Phe His Thr Gln Ser Glu Leu Ile Phe Asn Ala
325 330 335

Thr Arg Phe Glu Asn Asp Arg Val Phe Arg Cys Glu Ala Glu Asn Ile
340 345 350

Val Leu Gln Ile Asn Arg Glu Lys Pro Ile Ser Ser Ala Leu Thr Leu
355 360 365

Glu Val Leu Tyr Pro Pro Val Val Lys Val Ser Pro Ser Ala Ile Thr
370 375 380

Ala Asn Thr Ser Glu Ile Val Leu Leu Asn Cys Glu Tyr Phe Ala Asn
385 390 395 400

Pro Ala Ser Leu Thr Gln Val Glu Trp Tyr Arg Asn Asp Ile Leu Val
405 410 415

Asn Val Asn Asp Thr Thr His Tyr Lys Gly Gly Asn Ser Glu Asn Val
420 425 430

Ala Leu Val Ile Lys Ser Thr Glu Lys Glu Asp Ile Gly Asn Tyr Ser
435 440 445

Cys Gln Leu Ser Asn Asn Ile Gly Lys Gly Thr Ser Asp Gln Lys Ile
450 455 460

Asn Leu Asp Val Gln Tyr Ala Pro Thr Val Glu Ile Leu Met Ile Pro
465 470 475 480

Glu Gly Pro Val Lys Glu Ser Asp Glu Ser Asn Val Thr Leu Phe Cys
485 490 495

Asn Val Leu Asp Ala Asn Pro Ser Val Leu Thr Lys Val Arg Trp Tyr
500 505 510

Ala Asn Ser Thr Leu Leu Lys Glu Leu Pro Asp Cys Glu Glu Thr Arg
515 520 525

Glu Asp Leu Cys His Ile Asp Pro Ser Lys Leu Leu Leu Glu Ser Ile
530 535 540

Gly Arg Gly Phe Phe Tyr Asn Tyr Ser Cys Glu Gly Phe Asn Ala Ala
545 550 555 560

Gly Trp Gly Pro Arg Ser Glu Asp Lys Glu Leu Leu Val His Tyr Glu
565 570 575

Pro Gly Pro Ala Ala Leu Ser His Phe Pro Leu Val Ala Val Lys Lys
580 585 590

Lys Ser Val Thr Phe Ser Cys Ser Val Asp Asp Pro Gly Phe Pro Glu
595 600 605

Ser Asn Arg Phe Arg Trp Leu Arg Gly Gly Arg Gly Pro Leu Gln Asp
610 615 620

Ile Val Thr Lys Asp Trp Thr Val Glu Pro Val Gly Leu Asp Ser Arg
625 630 635 640

Thr Asn Tyr Ser Cys Tyr Ala Tyr Asn Glu Gly Gly Lys Gly Val Met
645 650 655

Ala Thr Val Asn Leu Glu Val His Ala Pro Pro Phe Phe Ile Lys Asn
660 665 670

Leu Pro Pro Tyr Thr Gly Ile Leu His Ser Ser Pro Asn Ala Thr Leu
675 680 685

Thr Cys Arg Ile Glu Cys Val Pro Arg Cys Asp Ile Ser Trp Gln Lys
690 695 700

Asp Gly Val Pro Ile Glu Arg Asn Asp Ser Arg Tyr Phe Ile Lys Glu
705 710 715 720

Asn Thr Trp Met Pro Pro Pro Gln Arg Glu Ile Leu Lys Ser Met Leu
725 730 735

Ser Val Leu His Phe Asn Met Pro Asn Trp Pro Asp Ser Lys Phe Asn
740 745 750

Ile Glu Ala Asp Asn Ala Asn Tyr Ser Cys Val Ser Thr Gly Asn Ile
755 760 765

Val Gly Gly Ser Ile Arg Ser Arg Thr Tyr Tyr Phe Gly Ile Glu Ala
770 775 780

Pro Glu Asn Thr Thr Val Ser Glu Asn Ile Val Tyr Val Gln Glu Asp
785 790 795 800

Thr Ile Pro Gly Arg Val Ile Cys Lys Ser Arg Ala Asn Pro Glu Pro
805 810 815

Ser Tyr Lys Trp Ile Phe Lys Asn Glu Thr Ile Ala Asn Gly Asn Ala
820 825 830

Leu Ile Ile Asn Thr Ala Met Asn Arg Asn Asp Asp Gly Thr Tyr Thr
835 840 845

Cys Leu Ala Tyr Asn Lys His Gly Ser Ser Ile Ala Lys Thr Val Ile
850 855 860

Lys Val Gln Phe Lys Pro Arg Cys Glu Ile Glu Arg Gln Glu Ile Asp
865 870 875 880

Asp Gln Asp Thr Leu Ile Cys Thr Ala Tyr Gly Asn Pro Ile Glu Ala
885 890 895

Asp Phe Ser Trp Ser Ile Lys Thr Glu Asn Glu Thr Asp Glu Asn Leu
900 905 910

Gly Ser Gly Lys Lys Glu Asn Ser Val Glu Lys Ser Phe Tyr Ile Leu
915 920 925

Gln Thr Asp Tyr Ala Ile Ser Arg Thr Tyr Arg Cys Val Ala Asn Asn
930 935 940

Thr Val Gly Tyr Gly Pro Phe Cys Glu Ile Glu Val Ala Glu Gln Leu
945 950 955 960

Ala Trp Trp Gln Leu Trp Glu Lys Asn Thr Leu Ile Ile Leu Val Ala
965 970 975

Ala Ile Leu Gly Leu Leu Leu Thr Val Ile Val Ile Cys Cys Ile Ile
980 985 990

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Arg Leu His
1010

<210> 66
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<212> PRT
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Met Arg Val His Tyr Leu Trp Leu Leu Leu Ile Leu Gly His Ala Ala
1 5 10 15

Ser Ala Gln Tyr Ser Ser Ala Asn Asp Trp Thr Val Asp His Pro Gln
20 25 30

Thr Leu Phe Ala Trp Glu Gly Ala Cys Ile Arg Ile Pro Cys Lys Tyr
35 40 45

Lys Thr Pro Leu Pro Lys Ala Arg Leu Asp Asn Ile Leu Leu Phe Gln
50 55 60

Asn Tyr Glu Phe Asp Lys Ala Thr Lys Lys Phe Lys Gly Thr Val Leu
65 70 75 80

Tyr Asn Lys Ala Glu Pro Glu Leu Tyr Pro Pro Lys Gln Arg Arg Val
85 90 95

Thr Phe Leu Gly Asn Ser Ile Asp Asn Cys Thr Leu Lys Ile His Pro
100 105 110

Ile Arg Ala Asn Asp Ser Gly Asn Leu Gly Leu Arg Met Thr Ala Gly
115 120 125

Thr Glu Arg Trp Met Glu Pro Ile His Leu Asn Val Ser Glu Lys Pro
130 135 140

Phe Gln Pro Tyr Ile Gln Met Pro Ser Glu Ile Arg Glu Ser Gln Ser
145 150 155 160

Val Thr Leu Thr Cys Gly Leu Asn Phe Ser Cys Phe Glu Tyr Asp Ile
165 170 175

Leu Leu Gln Trp Phe Leu Glu Asp Ser Lys Ile Thr Ser Val Thr Pro
180 185 190

Ser Val Thr Ser Ile Thr Ser Ser Val Thr Ser Ser Ile Lys Asn Val
195 200 205

Tyr Thr Glu Ser Lys Leu Thr Phe Gln Pro Lys Trp Thr Asp His Gly
210 215 220

Lys Ser Val Lys Cys Gln Val Gln His Ser Ser Glu Val Leu Ser Glu
225 230 235 240

Arg Thr Val Arg Leu Asp Val Lys Tyr Thr Pro Lys Leu Glu Ile Lys
245 250 255

Val Asn Pro Thr Glu Val Glu Lys Asn Asn Ser Val Thr Met Thr Cys
260 265 270

Arg Val Asn Ser Ser Asn Pro Lys Leu Arg Thr Val Ala Val Ser Trp
275 280 285

Phe Lys Asp Gly Arg Pro Leu Glu Asp Gln Glu Leu Glu Gln Glu Gln
290 295 300

Gln Met Ser Lys Leu Ile Leu His Ser Val Thr Lys Asp Met Arg Gly
305 310 315 320

Lys Tyr Arg Cys Gln Ala Ser Asn Asp Ile Gly Pro Gly Glu Ser Glu
325 330 335

Glu Val Glu Leu Thr Val His Tyr Ala Pro Glu Pro Ser Arg Val His
340 345 350

Ile Tyr Pro Ser Pro Ala Glu Glu Gly Gln Ser Val Glu Leu Ile Cys
355 360 365

Glu Ser Leu Ala Ser Pro Ser Ala Thr Asn Tyr Thr Trp Tyr His Asn
370 375 380

Arg Lys Pro Ile Pro Gly Asp Thr Gln Glu Lys Leu Arg Ile Pro Lys
385 390 395 400

Val Ser Pro Trp His Ala Gly Asn Tyr Ser Cys Leu Ala Glu Asn Arg
405 410 415

Leu Gly His Gly Lys Ile Asp Gln Glu Ala Lys Leu Asp Val His Tyr
420 425 430

Ala Pro Lys Ala Val Thr Thr Val Ile Gln Ser Phe Thr Pro Ile Leu
435 440 445

Glu Gly Asp Ser Val Thr Leu Val Cys Arg Tyr Asn Ser Ser Asn Pro
450 455 460

Asp Val Thr Ser Tyr Arg Trp Asn Pro Gln Gly Ser Gly Ser Val Leu
465 470 475 480

Lys Pro Gly Val Leu Arg Ile Gln Lys Val Thr Trp Asp Ser Met Pro
485 490 495

Val Ser Cys Ala Ala Cys Asn His Lys Cys Ser Trp Ala Leu Pro Val
500 505 510

Ile Leu Asn Val His Tyr Ala Pro Arg Asp Val Lys Val Leu Lys Val
515 520 525

Ser Pro Ala Ser Glu Ile Arg Ala Gly Gln Arg Val Leu Leu Gln Cys
530 535 540

Asp Phe Ala Glu Ser Asn Pro Ala Glu Val Arg Phe Phe Trp Lys Lys
545 550 555 560

Asn Gly Ser Leu Val Gln Glu Gly Arg Tyr Leu Ser Phe Gly Ser Val
565 570 575

Ser Pro Glu Asp Ser Gly Asn Tyr Asn Cys Met Val Asn Asn Ser Ile
580 585 590

Gly Glu Thr Leu Ser Gln Ala Trp Asn Leu Gln Val Leu Tyr Ala Pro
595 600 605

Arg Arg Leu Arg Val Ser Ile Ser Pro Gly Asp His Val Met Glu Gly
610 615 620

Lys Lys Ala Thr Leu Ser Cys Glu Ser Asp Ala Asn Pro Pro Ile Ser
625 630 635 640

Gln Tyr Thr Trp Phe Asp Ser Ser Gly Gln Asp Leu His Ser Ser Gly
 645 650 655

 Gln Lys Leu Arg Leu Glu Pro Leu Glu Val Gln His Thr Gly Ser Tyr
 660 665 670

 Arg Cys Lys Gly Thr Asn Gly Ile Gly Thr Gly Glu Ser Pro Pro Ser
 675 680 685

 Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Lys Arg Val Ala
 690 695 700

 Leu Gly Leu Gly Phe Cys Leu Thr Ile Cys Ile Leu Ala Ile Trp Gly
 705 710 715 720

 Met Lys Ile Gln Lys Lys Trp Lys Gln Asn Arg Ser Gln Gln Gly Leu
 725 730 735

 Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Ala
 740 745 750

 Arg Arg Thr Pro Leu Ser Glu Gly Pro Gln Ser Gln Gly Cys Tyr Asn
 755 760 765

 Pro Ala Met Asp Asp Thr Val Ser Tyr Ala Ile Leu Arg Phe Pro Glu
 770 775 780

 Ser Asp Met His Asn Ala Gly Asp Ala Gly Thr Pro Ala Thr Gln Ala
 785 790 795 800

 Pro Pro Pro Asn Asn Ser Asp Ser Val Thr Tyr Ser Val Ile Gln Lys
 805 810 815

 Arg Pro Met Gly Asp Tyr Glu Asn Val Asn Pro Ser Cys Pro Glu Asp
 820 825 830

 Glu Ser Ile His Tyr Ser Glu Leu Val Gln Phe Gly Ala Gly Lys Arg
 835 840 845

 Pro Gln Ala Lys Glu Asp Val Asp Tyr Val Thr Leu Lys His
 850 855 860

<210> 67
 <211> 1399
 <212> DNA
 <213> Homo sapiens

<400> 67

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agggacccc ctgcctcgat ccccatgatg cggccacat ggccgcctccg gcctctgcc 180
ccctctcccc acagatatcg acgagtgtcg catctctcct gacctctgcg gccaggac 240
ctgtgtcaac acgcccggca gctttgagtg cgagtgttt cccggctacg agagtggctt 300
catgctgatg aagaactgca tgggtcgggt actgcccggc aggggtgtgg tgggcgcct 360
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tggagggggc aggaggaggg aggagctgta aattagctga ggtacagtga gtctgggctc 480
catgaggcct cgtccttagg agagagacct gggcctgag acctggggtt ggcggcaca 540
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gctactcggg aggctgagga gggaggatcc cttagccca ggaggttgag gctgcagtga 1020
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<210> 68

<211> 2911

<212> PRT

<213> Homo sapiens

<400> 68

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Gly Cys Val Val Leu Trp Ala Gln Gly Thr Ala Gly Gln Pro Gln Pro
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Pro Pro Pro Lys Pro Pro Arg Pro Gln Pro Pro Pro Gln Gln Val Arg
35 40 45

Ser Ala Thr Ala Gly Ser Glu Gly Gly Phe Leu Ala Pro Glu Tyr Arg
50 55 60

Glu Glu Gly Ala Ala Val Ala Ser Arg Val Arg Arg Arg Gly Gln Gln
65 70 75 80

Asp Val Leu Arg Gly Pro Asn Val Cys Gly Ser Arg Phe His Ser Tyr		
85	90	95
Cys Cys Pro Gly Trp Lys Thr Leu Pro Gly Gly Asn Gln Cys Ile Val		
100	105	110
Pro Ile Cys Arg Asn Ser Cys Gly Asp Gly Phe Cys Ser Arg Pro Asn		
115	120	125
Met Cys Thr Cys Ser Ser Gly Gln Ile Ser Ser Thr Cys Gly Ser Lys		
130	135	140
Ser Ile Gln Gln Cys Ser Val Arg Cys Met Asn Gly Gly Thr Cys Ala		
145	150	155
Asp Asp His Cys Gln Cys Gln Lys Gly Tyr Ile Gly Thr Tyr Cys Gly		
165	170	175
Gln Pro Val Cys Glu Asn Gly Cys Gln Asn Gly Gly Arg Cys Ile Ala		
180	185	190
Gln Pro Cys Ala Cys Val Tyr Gly Phe Thr Gly Pro Gln Cys Glu Arg		
195	200	205
Asp Tyr Arg Thr Gly Pro Cys Phe Thr Gln Val Asn Asn Gln Met Cys		
210	215	220
Gln Gly Gln Leu Thr Gly Ile Val Cys Thr Lys Thr Leu Cys Cys Ala		
225	230	235
240		
Thr Thr Gly Arg Ala Trp Gly His Pro Cys Glu Met Cys Pro Ala Gln		
245	250	255
Pro Gln Pro Cys Arg Arg Gly Phe Ile Pro Asn Ile Arg Thr Gly Ala		
260	265	270
Cys Gln Asp Val Asp Glu Cys Gln Ala Ile Pro Gly Ile Cys Gln Gly		
275	280	285
Gly Asn Cys Ile Asn Thr Val Gly Ser Phe Glu Cys Arg Cys Pro Ala		
290	295	300
Gly His Lys Gln Ser Glu Thr Thr Gln Lys Cys Glu Asp Ile Asp Glu		
305	310	315
320		
Cys Ser Ile Ile Pro Gly Ile Cys Glu Thr Gly Glu Cys Ser Asn Thr		
325	330	335

Val Gly Ser Tyr Phe Cys Val Cys Pro Arg Gly Tyr Val Thr Ser Thr
340 345 350

Asp Gly Ser Arg Cys Ile Asp Gln Arg Thr Gly Met Cys Phe Ser Gly
355 360 365

Leu Val Asn Gly Arg Cys Ala Gln Glu Leu Pro Gly Arg Met Thr Lys
370 375 380

Met Gln Cys Cys Cys Glu Pro Gly Arg Cys Trp Gly Ile Gly Thr Ile
385 390 395 400

Pro Glu Ala Cys Pro Val Arg Gly Ser Glu Glu Tyr Arg Arg Leu Cys
405 410 415

Met Asp Gly Leu Pro Met Gly Gly Ile Pro Gly Ser Ala Gly Ser Arg
420 425 430

Pro Gly Gly Thr Gly Gly Asn Gly Phe Ala Pro Ser Gly Asn Gly Asn
435 440 445

Gly Tyr Gly Pro Gly Gly Thr Gly Phe Ile Pro Ile Pro Gly Gly Asn
450 455 460

Gly Phe Ser Pro Gly Val Gly Ala Gly Val Gly Ala Gly Gly Gln
465 470 475 480

Gly Pro Ile Ile Thr Gly Leu Thr Ile Leu Asn Gln Thr Ile Asp Ile
485 490 495

Cys Lys His His Ala Asn Leu Cys Leu Asn Gly Arg Cys Ile Pro Thr
500 505 510

Val Ser Ser Tyr Arg Cys Glu Cys Asn Met Gly Tyr Lys Gln Asp Ala
515 520 525

Asn Gly Asp Cys Ile Asp Val Asp Glu Cys Thr Ser Asn Pro Cys Thr
530 535 540

Asn Gly Asp Cys Val Asn Thr Pro Gly Ser Tyr Tyr Cys Lys Cys His
545 550 555 560

Ala Gly Phe Gln Arg Thr Pro Thr Lys Gln Ala Cys Ile Asp Ile Asp
565 570 575

Glu Cys Ile Gln Asn Gly Val Leu Cys Lys Asn Gly Arg Cys Val Asn
580 585 590

Ser Asp Gly Ser Phe Gln Cys Ile Cys Asn Ala Gly Phe Glu Leu Thr
595 600 605

Thr Asp Gly Lys Asn Cys Val Asp His Asp Glu Cys Thr Thr Thr Asn
610 615 620

Met Cys Leu Asn Gly Met Cys Ile Asn Glu Asp Gly Ser Phe Lys Cys
625 630 635 640

Ile Cys Lys Pro Gly Phe Val Leu Ala Pro Asn Gly Arg Tyr Cys Thr
645 650 655

Asp Val Asp Glu Cys Gln Thr Pro Gly Ile Cys Met Asn Gly His Cys
660 665 670

Ile Asn Ser Glu Gly Ser Phe Arg Cys Asp Cys Pro Pro Gly Leu Ala
675 680 685

Val Gly Met Asp Gly Arg Val Cys Val Asp Thr His Met Arg Ser Thr
690 695 700

Cys Tyr Gly Gly Ile Lys Lys Gly Val Cys Val Arg Pro Phe Pro Gly
705 710 715 720

Ala Val Thr Lys Ser Glu Cys Cys Ala Asn Pro Asp Tyr Gly Phe
725 730 735

Gly Glu Pro Cys Gln Pro Cys Pro Ala Lys Asn Ser Ala Glu Phe His
740 745 750

Gly Leu Cys Ser Ser Gly Val Gly Ile Thr Val Asp Gly Arg Asp Ile
755 760 765

Asn Glu Cys Ala Leu Asp Pro Asp Ile Cys Ala Asn Gly Ile Cys Glu
770 775 780

Asn Leu Arg Gly Ser Tyr Arg Cys Asn Cys Asn Ser Gly Tyr Glu Pro
785 790 795 800

Asp Ala Ser Gly Arg Asn Cys Ile Asp Ile Asp Glu Cys Leu Val Asn
805 810 815

Arg Leu Leu Cys Asp Asn Gly Leu Cys Arg Asn Thr Pro Gly Ser Tyr
820 825 830

Ser Cys Thr Cys Pro Pro Gly Tyr Val Phe Arg Thr Glu Thr Glu Thr
835 840 845

Cys Glu Asp Ile Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Ala
850 855 860

Cys Arg Asn Asn Leu Gly Ser Phe Asn Cys Glu Cys Ser Pro Gly Ser
865 870 875 880

Lys Leu Ser Ser Thr Gly Leu Ile Cys Ile Asp Ser Leu Lys Gly Thr
885 890 895

Cys Trp Leu Asn Ile Gln Asp Ser Arg Cys Glu Val Asn Ile Asn Gly
900 905 910

Ala Thr Leu Lys Ser Glu Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly
915 920 925

Ser Pro Cys Glu Arg Cys Glu Leu Asp Thr Ala Cys Pro Arg Gly Leu
930 935 940

Ala Arg Ile Lys Gly Val Thr Cys Glu Asp Val Asn Glu Cys Glu Val
945 950 955 960

Phe Pro Gly Val Cys Pro Asn Gly Arg Cys Val Asn Ser Lys Gly Ser
965 970 975

Phe His Cys Glu Cys Pro Glu Gly Leu Thr Leu Asp Gly Thr Gly Arg
980 985 990

Val Cys Leu Asp Ile Arg Met Glu Gln Cys Tyr Leu Lys Trp Asp Glu
995 1000 1005

Asp Glu Cys Ile His Pro Val Pro Gly Lys Phe Arg Met Asp Ala Cys
1010 1015 1020

Cys Cys Ala Val Gly Ala Ala Trp Gly Thr Glu Cys Glu Glu Cys Pro
1025 1030 1035 1040

Lys Pro Gly Thr Lys Glu Tyr Glu Thr Leu Cys Pro Arg Gly Ala Gly
1045 1050 1055

Phe Ala Asn Arg Gly Asp Val Leu Thr Gly Arg Pro Phe Tyr Lys Asp
1060 1065 1070

Ile Asn Glu Cys Lys Ala Phe Pro Gly Met Cys Thr Tyr Gly Lys Cys
1075 1080 1085

Arg Asn Thr Ile Gly Ser Phe Lys Cys Arg Cys Asn Ser Gly Phe Ala
1090 1095 1100

Leu Asp Met Glu Glu Arg Asn Cys Thr Asp Ile Asp Glu Cys Arg Ile
1105 1110 1115 1120

Ser Pro Asp Leu Cys Gly Ser Gly Ile Cys Val Asn Thr Pro Gly Ser
1125 1130 1135

Phe Glu Cys Glu Cys Phe Glu Gly Tyr Glu Ser Gly Phe Met Met Met
1140 1145 1150

Lys Asn Cys Met Asp Ile Asp Gly Cys Glu Arg Asn Pro Leu Leu Cys
1155 1160 1165

Arg Gly Gly Thr Cys Val Asn Thr Glu Gly Ser Phe Gln Cys Asp Cys
1170 1175 1180

Pro Leu Gly His Glu Leu Ser Pro Ser Arg Glu Asp Cys Val Asp Ile
1185 1190 1195 1200

Asn Glu Cys Ser Leu Ser Asp Asn Leu Cys Arg Asn Gly Lys Cys Val
1205 1210 1215

Asn Met Ile Gly Thr Tyr Gln Cys Ser Cys Asn Pro Gly Tyr Gln Ala
1220 1225 1230

Thr Pro Asp Arg Gln Gly Cys Thr Asp Ile Asp Glu Cys Met Ile Met
1235 1240 1245

Asn Gly Gly Cys Asp Thr Gln Cys Thr Asn Ser Glu Gly Ser Tyr Glu
1250 1255 1260

Cys Ser Cys Ser Glu Gly Tyr Ala Leu Met Pro Asp Gly Arg Ser Cys
1265 1270 1275 1280

Ala Asp Ile Asp Glu Cys Glu Asn Asn Pro Asp Ile Cys Asp Gly Gly
1285 1290 1295

Gln Cys Thr Asn Ile Pro Gly Glu Tyr Arg Cys Leu Cys Tyr Asp Gly
1300 1305 1310

Phe Met Ala Ser Met Asp Met Lys Thr Cys Ile Asp Val Asn Glu Cys
1315 1320 1325

Asp Leu Asn Ser Asn Ile Cys Met Phe Gly Glu Cys Glu Asn Thr Lys
1330 1335 1340

Gly Ser Phe Ile Cys His Cys Gln Leu Gly Tyr Ser Val Lys Lys Gly
1345 1350 1355 1360

Thr Thr Gly Cys Thr Asp Val Asp Glu Cys Glu Ile Gly Ala His Asn
1365 1370 1375

Cys Asp Met His Ala Ser Cys Leu Asn Ile Pro Gly Ser Phe Lys Cys
1380 1385 1390

Ser Cys Arg Glu Gly Trp Ile Gly Asn Gly Ile Lys Cys Ile Asp Leu
1395 1400 1405

Asp Glu Cys Ser Asn Gly Thr His Gln Cys Ser Ile Asn Ala Gln Cys
1410 1415 1420

Val Asn Thr Pro Gly Ser Tyr Arg Cys Ala Cys Ser Glu Gly Phe Thr
1425 1430 1435 1440

Gly Asp Gly Phe Thr Cys Ser Asp Val Asp Glu Cys Ala Glu Asn Ile
1445 1450 1455

Asn Leu Cys Glu Asn Gly Gln Cys Leu Asn Val Pro Gly Ala Tyr Arg
1460 1465 1470

Cys Glu Cys Glu Met Gly Phe Thr Pro Ala Ser Asp Ser Arg Ser Cys
1475 1480 1485

Gln Asp Ile Asp Glu Cys Ser Phe Gln Asn Ile Cys Val Ser Gly Thr
1490 1495 1500

Cys Asn Asn Leu Pro Gly Met Phe His Cys Ile Cys Asp Asp Gly Tyr
1505 1510 1515 1520

Glu Leu Asp Arg Thr Gly Gly Asn Cys Thr Asp Ile Asp Glu Cys Ala
1525 1530 1535

Asp Pro Ile Asn Cys Val Asn Gly Leu Cys Val Asn Thr Pro Gly Arg
1540 1545 1550

Tyr Glu Cys Asn Cys Pro Pro Asp Phe Gln Leu Asn Pro Thr Gly Val
1555 1560 1565

Gly Cys Val Asp Asn Arg Val Gly Asn Cys Tyr Leu Lys Phe Gly Pro
1570 1575 1580

Arg Gly Asp Gly Ser Leu Ser Cys Asn Thr Glu Ile Gly Val Gly Val
1585 1590 1595 1600

Ser Arg Ser Ser Cys Cys Ser Leu Gly Lys Ala Trp Gly Asn Pro
1605 1610 1615

Cys Glu Thr Cys Pro Pro Val Asn Ser Thr Glu Tyr Tyr Thr Leu Cys
 1620 1625 1630

 Pro Gly Gly Glu Gly Phe Arg Pro Asn Pro Ile Thr Ile Ile Leu Glu
 1635 1640 1645

 Asp Ile Asp Glu Cys Gln Glu Leu Pro Gly Leu Cys Gln Gly Gly Asn
 1650 1655 1660

 Cys Ile Asn Thr Phe Gly Ser Phe Gln Cys Glu Cys Pro Gln Gly Tyr
 1665 1670 1675 1680

 Tyr Leu Ser Glu Asp Thr Arg Ile Cys Glu Asp Ile Asp Glu Cys Phe
 1685 1690 1695

 Ala His Pro Gly Val Cys Gly Pro Gly Thr Cys Tyr Asn Thr Leu Gly
 1700 1705 1710

 Asn Tyr Thr Cys Ile Cys Pro Pro Glu Tyr Met Gln Val Asn Gly Gly
 1715 1720 1725

 His Asn Cys Met Asp Met Arg Lys Ser Phe Cys Tyr Arg Ser Tyr Asn
 1730 1735 1740

 Gly Thr Thr Cys Glu Asn Glu Leu Pro Phe Asn Val Thr Lys Arg Met
 1745 1750 1755 1760

 Cys Cys Cys Thr Tyr Asn Val Gly Lys 'Ala Gly Asn Lys Pro Cys Glu
 1765 1770 1775

 Pro Cys Pro Thr Pro Gly Thr Ala Asp Phe Lys Thr Ile Cys Gly Asn
 1780 1785 1790

 Ile Pro Gly Phe Thr Phe Asp Ile His Thr Gly Lys Ala Val Asp Ile
 1795 1800 1805

 Asp Glu Cys Lys Glu Ile Pro Gly Ile Cys Ala Asn Gly Val Cys Ile
 1810 1815 1820

 Asn Gln Ile Gly Ser Phe Arg Cys Glu Cys Pro Thr Gly Phe Ser Tyr
 1825 1830 1835 1840

 Asn Asp Leu Leu Val Cys Glu Asp Ile Asp Glu Cys Ser Asn Gly
 1845 1850 1855

 Asp Asn Leu Cys Gln Arg Asn Ala Asp Cys Ile Asn Ser Pro Gly Ser
 1860 1865 1870

Tyr Arg Cys Glu Cys Ala Ala Gly Phe Lys Leu Ser Pro Asn Gly Ala
1875 1880 1885

Cys Val Asp Arg Asn Glu Cys Leu Glu Ile Pro Asn Val Cys Ser His
1890 1895 1900

Gly Leu Cys Val Asp Leu Gln Gly Ser Tyr Gln Cys Ile Cys His Asn
1905 1910 1915 1920

Gly Phe Lys Ala Ser Gln Asp Gln Thr Met Cys Met Asp Val Asp Glu
1925 1930 1935

Cys Glu Arg His Pro Cys Gly Asn Gly Thr Cys Lys Asn Thr Val Gly
1940 1945 1950

Ser Tyr Asn Cys Leu Cys Tyr Pro Gly Phe Glu Leu Thr His Asn Asn
1955 1960 1965

Asp Cys Leu Asp Ile Asp Glu Cys Ser Ser Phe Phe Gly Gln Val Cys
1970 1975 1980

Arg Asn Gly Arg Cys Phe Asn Glu Ile Gly Ser Phe Lys Cys Leu Cys
1985 1990 1995 2000

Asn Glu Gly Tyr Glu Leu Thr Pro Asp Gly Lys Asn Cys Ile Asp Thr
2005 2010 2015

Asn Glu Cys Val Ala Leu Pro Gly Ser Cys Ser Pro Gly Thr Cys Gln
2020 2025 2030

Asn Leu Glu Gly Ser Phe Arg Cys Ile Cys Pro Pro Gly Tyr Glu Val
2035 2040 2045

Lys Ser Glu Asn Cys Ile Asp Ile Asn Glu Cys Asp Glu Asp Pro Asn
2050 2055 2060

Ile Cys Leu Phe Gly Ser Cys Thr Asn Thr Pro Gly Gly Phe Gln Cys
2065 2070 2075 2080

Leu Cys Pro Pro Gly Phe Val Leu Ser Asp Asn Gly Arg Arg Cys Phe
2085 2090 2095

Asp Thr Arg Gln Ser Phe Cys Phe Thr Asn Phe Glu Asn Gly Lys Cys
2100 2105 2110

Ser Val Pro Lys Ala Phe Asn Thr Thr Lys Ala Lys Cys Cys Cys Ser
2115 2120 2125

Lys Met Pro Gly Glu Gly Trp Gly Asp Pro Cys Glu Leu Cys Pro Lys
2130 2135 2140

Asp Asp Glu Val Ala Phe Gln Asp Leu Cys Pro Tyr Gly His Gly Thr
2145 2150 2155 2160

Val Pro Ser Leu His Asp Thr Arg Glu Asp Val Asn Glu Cys Leu Glu
2165 2170 2175

Ser Pro Gly Ile Cys Ser Asn Gly Gln Cys Ile Asn Thr Asp Gly Ser
2180 2185 2190

Phe Arg Cys Glu Cys Pro Met Gly Tyr Asn Leu Asp Tyr Thr Gly Val
2195 2200 2205

Arg Cys Val Asp Thr Asp Glu Cys Ser Ile Gly Asn Pro Cys Gly Asn
2210 2215 2220

Gly Thr Cys Thr Asn Val Ile Gly Ser Phe Glu Cys Asn Cys Asn Glu
2225 2230 2235 2240

Gly Phe Glu Pro Gly Pro Met Met Asn Cys Glu Asp Ile Asn Glu Cys
2245 2250 2255

Ala Gln Asn Pro Leu Leu Cys Ala Leu Arg Cys Met Asn Thr Phe Gly
2260 2265 2270

Ser Tyr Glu Cys Thr Cys Pro Ile Gly Tyr Ala Leu Arg Glu Asp Gln
2275 2280 2285

Lys Met Cys Lys Asp Leu Asp Glu Cys Ala Glu Gly Leu His Asp Cys
2290 2295 2300

Glu Ser Arg Gly Met Met Cys Lys Asn Leu Ile Gly Thr Phe Met Cys
2305 2310 2315 2320

Ile Cys Pro Pro Gly Met Ala Arg Arg Pro Asp Gly Glu Gly Cys Val
2325 2330 2335

Asp Glu Asn Glu Cys Arg Thr Lys Pro Gly Ile Cys Glu Asn Gly Arg
2340 2345 2350

Cys Val Asn Ile Ile Gly Ser Tyr Arg Cys Glu Cys Asn Glu Gly Phe
2355 2360 2365

Gln Ser Ser Ser Ser Gly Thr Glu Cys Leu Asp Asn Arg Gln Gly Leu
2370 2375 2380

Cys Phe Ala Glu Val Leu Gln Thr Ile Cys Gln Met Ala Ser Ser Ser
2385 2390 2395 2400

Arg Asn Leu Val Thr Lys Ser Glu Cys Cys Cys Asp Gly Gly Arg Gly
2405 2410 2415

Trp Gly His Gln Cys Glu Leu Cys Pro Leu Pro Gly Thr Ala Gln Tyr
2420 2425 2430

Lys Lys Ile Cys Pro His Gly Pro Gly Tyr Thr Thr Asp Gly Arg Asp
2435 2440 2445

Ile Asp Glu Cys Lys Val Met Pro Asn Leu Cys Thr Asn Gly Gln Cys
2450 2455 2460

Ile Asn Thr Met Gly Ser Phe Arg Cys Phe Cys Lys Val Gly Tyr Thr
2465 2470 2475 2480

Thr Asp Ile Ser Gly Thr Ser Cys Ile Asp Leu Asp Glu Cys Ser Gln
2485 2490 2495

Ser Pro Lys Pro Cys Asn Tyr Ile Cys Lys Asn Thr Glu Gly Ser Tyr
2500 2505 2510

Gln Cys Ser Cys Pro Arg Gly Tyr Val Leu Gln Glu Asp Gly Lys Thr
2515 2520 2525

Cys Lys Asp Leu Asp Glu Cys Gln Thr Lys Gln His Asn Cys Gln Phe
2530 2535 2540

Leu Cys Val Asn Thr Leu Gly Gly Phe Thr Cys Lys Cys Pro Pro Gly
2545 2550 2555 2560

Phe Thr Gln His His Thr Ala Cys Ile Asp Asn Asn Glu Cys Gly Ser
2565 2570 2575

Gln Pro Leu Leu Cys Gly Gly Lys Gly Ile Cys Gln Asn Thr Pro Gly
2580 2585 2590

Ser Phe Ser Cys Glu Cys Gln Arg Gly Phe Ser Leu Asp Ala Thr Gly
2595 2600 2605

Leu Asn Cys Glu Asp Val Asp Glu Cys Asp Gly Asn His Arg Cys Gln
2610 2615 2620

His Gly Cys Gln Asn Ile Leu Gly Gly Tyr Arg Cys Gly Cys Pro Gln
2625 2630 2635 2640

Gly Tyr Ile Gln His Tyr Gln Trp Asn Gln Cys Val Asp Glu Asn Glu
2645 2650 2655

Cys Ser Asn Pro Asn Ala Cys Gly Ser Ala Ser Cys Tyr Asn Thr Leu
2660 2665 2670

Gly Ser Tyr Lys Cys Ala Cys Pro Ser Gly Phe Ser Phe Asp Gln Phe
2675 2680 2685

Ser Ser Ala Cys His Asp Val Asn Glu Cys Ser Ser Ser Lys Asn Pro
2690 2695 2700

Cys Asn Tyr Gly Cys Ser Asn Thr Glu Gly Gly Tyr Leu Cys Gly Cys
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Pro Pro Gly Tyr Tyr Arg Val Gly Gln Gly His Cys Val Ser Gly Met
2725 2730 2735

Gly Phe Asn Lys Gly Gln Tyr Leu Ser Leu Asp Thr Glu Val Asp Glu
2740 2745 2750

Glu Asn Ala Leu Ser Pro Glu Ala Cys Tyr Glu Cys Lys Ile Asn Gly
2755 2760 2765

Tyr Pro Lys Lys Asp Ser Arg Gln Lys Arg Ser Ile His Glu Pro Asp
2770 2775 2780

Pro Thr Ala Val Glu Gln Ile Ser Leu Glu Ser Val Asp Met Asp Ser
2785 2790 2795 2800

Pro Val Asn Met Lys Phe Asn Leu Ser His Leu Gly Ser Lys Glu His
2805 2810 2815

Ile Leu Glu Leu Arg Pro Ala Ile Gln Pro Leu Asn Asn His Ile Arg
2820 2825 2830

Tyr Val Ile Ser Gln Gly Asn Asp Asp Ser Val Phe Arg Ile His Gln
2835 2840 2845

Arg Asn Gly Leu Ser Tyr Leu His Thr Ala Lys Lys Lys Leu Met Pro
2850 2855 2860

Gly Thr Tyr Thr Leu Glu Ile Thr Ser Ile Pro Leu Tyr Lys Lys Lys
2865 2870 2875 2880

Glu Leu Lys Lys Leu Glu Ser Asn Glu Asp Asp Tyr Leu Leu Gly
2885 2890 2895

Glu Leu Gly Glu Ala Leu Arg Met Arg Leu Gln Ile Gln Leu Tyr
2900 2905 2910

<210> 69
<211> 2135
<212> DNA
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<400> 69

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taccgctgtg tccgggtggg tggtcagaat gccgtgctcc aggtgtcac agctgcttcg 240
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caccactcag tatatgtgag ggagggatgt gcctctggcc acgtggttac ctigcagtgc 480
acagcctgtg gtcataagaag gggctacagc tcacgcatacg tgggtgaaa catgtccttg 540
ctctcgcaatgc ggccttggca ggccagcctt cagttccagg gctaccaccc gtgcggggc 600
tctgtcatca cgcggctgtg gatcatcaact gtcacact gtgttatga ctgttacctc 660
cccaagtcat ggaccatcca ggtgggtcta gttccctgt tggacaatcc agccccatcc 720
cacttggtg agaagattgt ctaccacagc aagtacaagc caaagaggct gggcaatgac 780
atcgccccta tgaagctggc cgggcccactc acgttcaatg aaatgatcca gcctgtgtgc 840
ctgccaact ctgaagagaa cttcccccgtt ggaaaagtgt gctggacgac aggatggggg 900
gccacagagg atggagcagg tgacgcctcc cctgtcctga accacgcggc cgccctttg 960
atttccaaca agatctgcaaa ccacaggagc gtgtacgggt gcatcatctc cccctccatg 1020
ctctgcgcgg gtcacctgac gggtggcggt gacagctgcc agggggacag cggggggccc 1080
ctgggtgtgc aagagaggag gctgtggaaat ttagtggag cgaccagctt tggcatggc 1140
tgcgcagagg tgaacaagcc tgggtgtac acccggtca cctccttcct ggactggatc 1200
cacgagcaga tggagagaga cctaaaaacc tgaagaggaa ggggacaagt agccacctga 1260
gttcctgagg ttagtgcac agcccgatcc tccctggac tcccggttagt gaacctgcac 1320
acgagcagac acccttggag ctctgagttc cggcaccagt agcaggcccg aaagaggcac 1380
ccttccatct gattccagca caaccttcaa gctgttttt gtttttgggt tttttgaggt 1440
ggagtctcgc tctgttgcggc aggctggagt gcagtggcga aatccctgct cactgcagcc 1500
tccgcttccc tgggtcaagc gattctttc cctcagcttc cccagtagct gggaccacag 1560
gtgcccgc当地 ccacacccaa ctaattttt tatttttagt agagacaggg tttcaccatg 1620
ttggccagggc tgctctcaaa cccctgaccc caaatgtgt gctgttca gcctcccaca 1680
gtgctggat tacaggcatg ggccaccacg cctagcctca cgctccttcc ttagtgcac 1740
taagaacaaa agaagcagca acttgcagg ggcgccttc ccactggtcc atctggttt 1800
ctctccaggg gtcttgcaaa attcctgacg agataagcag ttatgtgacc tcacgtgcaa 1860
agccaccaac agccactcag aaaagacgca ccagccaga agtgcagaac tgcaact 1920
gcacgttttc atctcttaggg accagaacca aaccacccct ttctacttcc aagacttatt 1980
ttcacatgtg gggaggttaa tcttaggaatg actcgtaaa ggcctattt catgatttct 2040
ttgttagcatt tgggtgcttga cgtattatttgc tcccttgatt ccaaataata tggcccttc 2100
cctcaaaaaaaaaaaaaaaaaaaaaaaa aaaaaaaa 2135

<210> 70
<211> 790
<212> PRT
<213> Sus scrofa

<400> 70
Asp Ser Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Phe Leu Phe Ser
1 5 10 15

Leu Ser Arg Lys Gln Val Ala Ala Arg Ser Val Glu Glu Cys Ala Ala
20 25 30

Lys Cys Glu Ala Glu Thr Asn Phe Ile Cys Arg Ala Phe Gln Tyr His
35 40 45

Ser Lys Asp Gln Gln Cys Val Val Met Ala Glu Asn Ser Lys Thr Ser
50 55 60

Pro Ile Ala Arg Met Arg Asp Val Val Leu Phe Glu Lys Arg Ile Tyr
65 70 75 80

Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr Thr
85 90 95

Ser Lys Thr Lys Ser Gly Val Ile Cys Gln Lys Trp Ser Val Ser Ser
100 105 110

Pro His Ile Pro Lys Tyr Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu
115 120 125

Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Lys Gly Pro Trp
130 135 140

Cys Tyr Thr Thr Asp Pro Glu Thr Arg Phe Asp Tyr Cys Asp Ile Pro
145 150 155 160

Glu Cys Glu Asp Glu Cys Met His Cys Ser Gly Glu His Tyr Glu Gly
165 170 175

Lys Ile Ser Lys Thr Met Ser Gly Ile Glu Cys Gln Ser Trp Gly Ser
180 185 190

Gln Ser Pro His Ala His Gly Tyr Leu Pro Ser Lys Phe Pro Asn Lys
195 200 205

Asn Leu Lys Met Asn Tyr Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro
210 215 220

Trp	Cys	Phe	Thr	Thr	Asp	Pro	Asn	Lys	Arg	Trp	Glu	Phe	Cys	Asp	Ile
225															240
Pro	Arg	Cys	Thr	Thr	Pro	Pro	Pro	Thr	Ser	Gly	Pro	Thr	Tyr	Gln	Cys
															255
Leu	Lys	Gly	Arg	Gly	Glu	Asn	Tyr	Arg	Gly	Thr	Val	Ser	Val	Thr	Ala
															260
265															270
Ser	Gly	His	Thr	Cys	Gln	Arg	Trp	Ser	Ala	Gln	Ser	Pro	His	Lys	His
															275
280															285
Asn	Arg	Thr	Pro	Glu	Asn	Phe	Pro	Cys	Lys	Asn	Leu	Glu	Glu	Asn	Tyr
															290
295															300
Cys	Arg	Asn	Pro	Asp	Gly	Glu	Thr	Ala	Pro	Trp	Cys	Tyr	Thr	Thr	Asp
															305
310															320
Ser	Glu	Val	Arg	Trp	Asp	Tyr	Cys	Lys	Ile	Pro	Ser	Cys	Gly	Ser	Ser
															325
330															335
Thr	Thr	Ser	Thr	Glu	His	Leu	Asp	Ala	Pro	Val	Pro	Pro	Glu	Gln	Thr
															340
345															350
Pro	Val	Ala	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Glu	Ser	Tyr	Arg	Gly
															355
360															365
Thr	Ser	Ser	Thr	Thr	Ile	Thr	Gly	Arg	Lys	Cys	Gln	Ser	Trp	Val	Ser
															370
375															380
Met	Thr	Pro	His	Arg	His	Glu	Lys	Thr	Pro	Gly	Asn	Phe	Pro	Asn	Ala
															385
390															400
Gly	Leu	Thr	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Asp	Lys	Ser	Pro
															405
410															415
Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Arg	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu
															420
425															430
Lys	Lys	Cys	Ser	Glu	Thr	Glu	Gln	Gln	Val	Thr	Asn	Phe	Pro	Ala	Ile
															435
440															445
Ala	Gln	Val	Pro	Ser	Val	Glu	Asp	Leu	Ser	Glu	Asp	Cys	Met	Phe	Gly
															450
455															460
Asn	Gly	Lys	Arg	Tyr	Arg	Gly	Lys	Arg	Ala	Thr	Thr	Val	Ala	Gly	Val
															465
470															480
475															

Pro Cys Gln Glu Trp Ala Ala Gln Glu Pro His Arg His Ser Ile Phe
 485 490 495

Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys Asn Tyr Cys Arg
 500 505 510

Asn Pro Asp Gly Asp Asp Asn Gly Pro Trp Cys Tyr Thr Thr Asn Pro
 515 520 525

Gln Lys Leu Phe Asp Tyr Cys Asp Val Pro Gln Cys Val Thr Ser Ser
 530 535 540

Phe Asp Cys Gly Lys Pro Lys Val Glu Pro Lys Lys Cys Pro Ala Arg
 545 550 555 560

Val Val Gly Gly Cys Val Ser Ile Pro His Ser Trp Pro Trp Gln Ile
 565 570 575

Ser Leu Arg Tyr Arg Gly His Phe Cys Gly Gly Thr Leu Ile
 580 585 590

Ser Pro Glu Trp Val Leu Thr Ala Lys His Cys Leu Glu Lys Ser Ser
 595 600 605

Ser Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Glu Glu Tyr His
 610 615 620

Leu Gly Glu Gly Val Gln Glu Ile Asp Val Ser Lys Leu Phe Lys Glu
 625 630 635 640

Pro Ser Glu Ala Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val
 645 650 655

Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Thr Pro Asn Tyr Val
 660 665 670

Val Ala Asp Arg Thr Ala Cys Tyr Ile Thr Gly Trp Gly Glu Thr Lys
 675 680 685

Gly Thr Tyr Gly Ala Gly Leu Leu Lys Glu Ala Arg Leu Pro Val Ile
 690 695 700

Glu Asn Lys Val Cys Asn Arg Tyr Glu Tyr Leu Gly Gly Lys Val Ser
 705 710 715 720

Pro Asn Glu Leu Cys Ala Gly His Leu Ala Gly Gly Ile Asp Ser Cys
 725 730 735

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr
740 745 750

Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Leu Pro Asn
755 760 765

Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu
770 775 780

Glu Ile Met Arg Arg Asn
785 790

<210> 71
<211> 812
<212> PRT
<213> Bos taurus

<400> 71
Met Leu Pro Ala Ser Pro Lys Met Glu His Lys Ala Val Val Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Lys Ser Gly Leu Gly Asp Leu Leu Asp Asp Tyr
20 25 30

Val Asn Thr Gln Gly Ala Ser Leu Leu Ser Leu Ser Arg Lys Asn Leu
35 40 45

Ala Gly Arg Ser Val Glu Asp Cys Ala Ala Lys Cys Glu Glu Glu Thr
50 55 60

Asp Phe Val Cys Arg Ala Phe Gln Tyr His Ser Lys Glu Gln Gln Cys
65 70 75 80

Val Val Met Ala Glu Asn Ser Lys Asn Thr Pro Val Phe Arg Met Arg
85 90 95

Asp Val Ile Leu Tyr Glu Lys Arg Ile Tyr Leu Leu Glu Cys Lys Thr
100 105 110

Gly Asn Gly Gln Thr Tyr Arg Gly Thr Thr Ala Glu Thr Lys Ser Gly
115 120 125

Val Thr Cys Gln Lys Trp Ser Ala Thr Ser Pro His Val Pro Lys Phe
130 135 140

Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu Glu Glu Asn Tyr Cys Arg

145	150	155	160
Asn Pro Asp Asn Asp Glu Asn Gly Pro Trp Cys Tyr Thr Thr Asp Pro			
165	170	175	
Asp Lys Arg Tyr Asp Tyr Cys Asp Ile Pro Glu Cys Glu Asp Lys Cys			
180	185	190	
Met His Cys Ser Gly Glu Asn Tyr Glu Gly Lys Ile Ala Lys Thr Met			
195	200	205	
Ser Gly Arg Asp Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala His			
210	215	220	
Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys Asn Leu Lys Met Asn Tyr			
225	230	235	240
Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro Trp Cys Phe Thr Thr Asp			
245	250	255	
Pro Gln Lys Arg Trp Glu Phe Cys Asp Ile Pro Arg Cys Thr Thr Pro			
260	265	270	
Pro Pro Ser Ser Gly Pro Lys Tyr Gln Cys Leu Lys Gly Thr Gly Lys			
275	280	285	
Asn Tyr Gly Gly Thr Val Ala Val Thr Glu Ser Gly His Thr Cys Gln			
290	295	300	
Arg Trp Ser Glu Gln Thr Pro His Lys His Asn Arg Thr Pro Glu Asn			
305	310	315	320
Phe Pro Cys Lys Asn Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asn Gly			
325	330	335	
Glu Lys Ala Pro Trp Cys Tyr Thr Asn Ser Glu Val Arg Trp Glu			
340	345	350	
Tyr Cys Thr Ile Pro Ser Cys Glu Ser Ser Pro Leu Ser Thr Glu Arg			
355	360	365	
Met Asp Val Pro Val Pro Pro Glu Gln Thr Pro Val Pro Gln Asp Cys			
370	375	380	
Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly Thr Ser Ser Thr Thr Ile			
385	390	395	400
Thr Gly Arg Lys Cys Gln Ser Trp Ser Ser Met Thr Pro His Arg His			

	405	410	415
Leu Lys Thr Pro Glu Asn Tyr Pro Asn Ala Gly Leu Thr Met Asn Tyr			
420	425	430	
Cys Arg Asn Pro Asp Ala Asp Lys Ser Pro Trp Cys Tyr Thr Thr Asp			
435	440	445	
Pro Arg Val Arg Trp Glu Phe Cys Asn Leu Lys Lys Cys Ser Glu Thr			
450	455	460	
Pro Glu Gln Val Pro Ala Ala Pro Gln Ala Pro Gly Val Glu Asn Pro			
465	470	475	480
Pro Glu Ala Asp Cys Met Ile Gly Thr Gly Lys Ser Tyr Arg Gly Lys			
485	490	495	
Lys Ala Thr Thr Val Ala Gly Val Pro Cys Gln Glu Trp Ala Ala Gln			
500	505	510	
Glu Pro His Gln His Ser Ile Phe Thr Pro Glu Thr Asn Pro Gln Ser			
515	520	525	
Gly Leu Glu Arg Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Asn Gly			
530	535	540	
Pro Trp Cys Tyr Thr Met Asn Pro Arg Lys Pro Phe Asp Tyr Cys Asp			
545	550	555	560
Val Pro Gln Cys Glu Ser Ser Phe Asp Cys Gly Lys Pro Lys Val Glu			
565	570	575	
Pro Lys Lys Cys Ser Gly Arg Ile Val Gly Gly Cys Val Ser Lys Pro			
580	585	590	
His Ser Trp Pro Trp Gln Val Ser Leu Arg Arg Ser Ser Arg His Phe			
595	600	605	
Cys Gly Gly Thr Leu Ile Ser Pro Lys Trp Val Leu Thr Ala Ala His			
610	615	620	
Cys Leu Asp Asn Ile Leu Ala Leu Ser Phe Tyr Lys Val Ile Leu Gly			
625	630	635	640
Ala His Asn Glu Lys Val Arg Glu Gln Ser Val Gln Glu Ile Pro Val			
645	650	655	
Ser Arg Leu Phe Arg Glu Pro Ser Gln Ala Asp Ile Ala Leu Leu Lys			

660 665 670
Leu Ser Arg Pro Ala Ile Ile Thr Lys Glu Val Ile Pro Ala Cys Leu
675 680 685

Pro Pro Pro Asn Tyr Met Val Ala Ala Arg Thr Glu Cys Tyr Ile Thr
690 695 700

Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Glu Gly Leu Leu Lys Glu
705 710 715 720

Ala His Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Asn Glu Tyr
725 730 735

Leu Asp Gly Arg Val Lys Pro Thr Glu Leu Cys Ala Gly His Leu Ile
740 745 750

Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
755 760 765

Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu
770 775 780

Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Pro
785 790 795 800

Tyr Val Pro Trp Ile Glu Glu Thr Met Arg Arg Asn
805 810

<210> 72
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Consensus
Sequence

<400> 72
Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser
20 25 30

Leu Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly
35 40 45

Ser	Asp	Ser	Ser	Ile	Arg	Val	Arg	Leu	Gly	Ser	His	Asp	Leu	Ser	Ser
50				55						60					
Gly	Glu	Glu	Thr	Gln	Thr	Val	Lys	Val	Ser	Lys	Val	Ile	Val	His	Pro
65				70					75				80		
Asn	Tyr	Asn	Pro	Ser	Thr	Tyr	Asp	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu
				85				90					95		
Lys	Glu	Pro	Val	Thr	Leu	Ser	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro
			100				105				110				
Ser	Ser	Gly	Tyr	Asn	Val	Pro	Ala	Gly	Thr	Thr	Cys	Thr	Val	Ser	Gly
		115				120				125					
Trp	Gly	Arg	Thr	Ser	Glu	Ser	Gly	Gly	Ser	Leu	Pro	Asp	Thr	Leu	Gln
		130			135				140						
Glu	Val	Asn	Val	Pro	Ile	Val	Ser	Asn	Ala	Thr	Cys	Arg	Arg	Ala	Tyr
145				150				155				160			
Ser	Gly	Gly	Ala	Ile	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Gly	Leu	Glu
		165					170				175				
Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys
		180				185				190					
Asn	Asp	Asn	Arg	Trp	Val	Leu	Val	Gly	Ile	Val	Ser	Trp	Gly	Ser	Asp
		195				200				205					
Gly	Cys	Ala	Arg	Pro	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	Ser
		210			215				220						
Tyr	Leu	Asp	Trp	Ile											
		225													

<210> 73

<211> 2646

<212> DNA

<213> Homo sapiens

<400> 73

atcagcaaca attaaaatat tcacgtgta tctgtagttt aataatggac caacatcaac 60
 atttgaataa aacagcagag tcagcatctt cagagaaaaaa gaaaacaaga cgctgcaatg 120
 gattcaagat gttcttggca gccctgtcat tcaagctatat tgctaaagca ctaggtggaa 180
 tcatttatgaa aatttccatc actcaaatacg aaaggagatt tgacatatcc tcttcttttg 240

<210> 74
<211> 691
<212> PRT
<213> *Homo sapiens*

<400> 74

Met	Asp	Gln	Asn	Gln	His	Leu	Asn	Lys	Thr	Ala	Glu	Ala	Gln	Pro	Ser
1					5				10					15	
Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala															
		20				25				30					
Ala	Leu	Ser	Leu	Ser	Phe	Ile	Ala	Lys	Thr	Leu	Gly	Ala	Ile	Ile	Met
		35				40				45					
Lys	Ser	Ser	Ile	Ile	His	Ile	Glu	Arg	Arg	Phe	Glu	Ile	Ser	Ser	Ser
		50				55				60					
Leu	Val	Gly	Phe	Ile	Asp	Gly	Ser	Phe	Glu	Ile	Gly	Asn	Leu	Leu	Val
	65			70				75				80			
Ile	Val	Phe	Val	Ser	Tyr	Phe	Gly	Ser	Lys	Leu	His	Arg	Pro	Lys	Leu
		85				90				95					
Ile	Gly	Ile	Gly	Cys	Phe	Ile	Met	Gly	Ile	Gly	Gly	Val	Leu	Thr	Ala
		100				105				110					
Leu	Pro	His	Phe	Phe	Met	Gly	Tyr	Tyr	Arg	Tyr	Ser	Lys	Glu	Thr	Asn
	115			120				125							
Ile	Asn	Ser	Ser	Glu	Asn	Ser	Thr	Ser	Thr	Leu	Ser	Thr	Cys	Leu	Ile
	130			135				140							
Asn	Gln	Ile	Leu	Ser	Leu	Asn	Arg	Ala	Ser	Pro	Glu	Ile	Val	Gly	Lys
	145			150				155				160			
Gly	Cys	Leu	Lys	Glu	Ser	Gly	Ser	Tyr	Met	Trp	Ile	Tyr	Val	Phe	Met
	165			170				175							
Gly	Asn	Met	Leu	Arg	Gly	Ile	Gly	Glu	Thr	Pro	Ile	Val	Pro	Leu	Gly
		180				185			190						
Leu	Ser	Tyr	Ile	Asp	Asp	Phe	Ala	Lys	Glu	Gly	His	Ser	Ser	Leu	Tyr
	195			200				205							
Leu	Gly	Ile	Leu	Asn	Ala	Ile	Ala	Met	Ile	Gly	Pro	Ile	Ile	Gly	Phe
	210			215				220							
Thr	Leu	Gly	Ser	Leu	Phe	Ser	Lys	Met	Tyr	Val	Asp	Ile	Gly	Tyr	Val
	225			230				235				240			
Asp	Leu	Ser	Thr	Ile	Arg	Ile	Thr	Pro	Thr	Asp	Ser	Arg	Trp	Val	Gly
		245				250			255						

Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
260 265 270

Ser Ile Pro Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
275 280 285

Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
290 295 300

Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
305 310 315 320

Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
325 330 335

Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
340 345 350

Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
355 360 365

Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
370 375 380

Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe
385 390 395 400

Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val
405 410 415

Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn
420 425 430

Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
435 440 445

Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
450 455 460

Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
465 470 475 480

Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
485 490 495

Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
500 505 510

Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp		
515	520	525
Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn		
530	535	540
Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val		
545	550	555
Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser		
565	570	575
Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly		
580	585	590
Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly		
595	600	605
Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val		
610	615	620
Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr		
625	630	635
Ile Ile Leu Ile Tyr Ala Met Lys Lys Tyr Gln Glu Lys Asp Ile		
645	650	655
Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser		
660	665	670
Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu		
675	680	685
Thr His Cys		
690		

<210> 75
<211> 204
<212> DNA
<213> Rattus norvegicus

<400> 75
ggctgaggag gaggcggcgg cagcggagtt gcgtggagaa cacacgctca ctgagaagtt 60
tgtctgcttg gatcaactcct tcgggcatga ctgcagccta acctgcgtatg actgcaggaa 120
tggggggact tgctcccggt gccaggacgg ctgtgactgc ccagagggt ggactggaat 180
catctgcaat gagacttgtc ctcc 204

<210> 76
<211> 91
<212> DNA
<213> Rattus norvegicus

<400> 76
tggtggacct gcatggccgg ctgcctttg tgccggccct gccccacatt gcggtgctga 60
ggatgagct gcccgactc ttccaggatg a 91

<210> 77
<211> 1574
<212> PRT
<213> Rattus norvegicus

<400> 77
Met Pro Val Arg Ala Glu Ala Arg Ala Ala Trp Arg Val Val Ala Leu
1 5 10 15

Ala Leu Leu Leu Leu Pro Ala Met Pro Ala Ala Ser Pro Pro Leu Thr
20 25 30

Pro Arg Pro Leu Gln Pro Ser Met Pro His Val Cys Ala Glu Gln Lys
35 40 45

Leu Thr Leu Val Gly His Arg Gln Pro Cys Val Gln Ala Phe Ser Arg
50 55 60

Ile Val Pro Val Trp Arg Arg Thr Gly Cys Ala Gln Gln Ala Trp Cys
65 70 75 80

Ile Gly Gln Glu Arg Arg Thr Val Tyr Tyr Met Ser Tyr Arg Gln Val
85 90 95

Tyr Ala Thr Glu Ala Arg Thr Val Phe Arg Cys Cys Pro Gly Trp Ser
100 105 110

Gln Lys Pro Gly Gln Glu Gly Cys Leu Ser Asp Val Asp Glu Cys Ala
115 120 125

Ser Ala Asn Gly Gly Cys Glu Gly Pro Cys Cys Asn Thr Val Gly Gly
130 135 140

Phe Tyr Cys Arg Cys Pro Pro Gly Tyr Gln Leu Gln Gly Asp Gly Lys
145 150 155 160

Thr Cys Gln Asp Val Asp Glu Cys Arg Ala His Asn Gly Gly Cys Gln
165 170 175

His Arg Cys Val Asn Thr Pro Gly Ser Tyr Leu Cys Glu Cys Lys Pro
180 185 190

Gly Phe Arg Leu His Thr Asp Gly Arg Thr Cys Leu Ala Ile Ser Ser
195 200 205

Cys Thr Leu Gly Asn Gly Gly Cys Gln His Gln Cys Val Gln Leu Thr
210 215 220

Val Thr Gln His Arg Cys Gln Cys Arg Pro Gln Tyr Gln Leu Gln Glu
225 230 235 240

Asp Gly Arg Arg Cys Val Arg Arg Ser Pro Cys Ala Glu Gly Asn Gly
245 250 255

Gly Cys Met His Ile Cys Gln Glu Leu Arg Gly Leu Ala His Cys Gly
260 265 270

Cys His Pro Gly Tyr Gln Leu Ala Ala Asp Arg Lys Thr Cys Glu Asp
275 280 285

Val Asp Glu Cys Ala Leu Gly Leu Ala Gln Cys Ala His Gly Cys Leu
290 295 300

Asn Thr Gln Gly Ser Phe Lys Cys Val Cys His Ala Gly Tyr Glu Leu
305 310 315 320

Gly Ala Asp Gly Arg Gln Cys Tyr Arg Ile Glu Met Glu Ile Val Asn
325 330 335

Ser Cys Glu Ala Gly Asn Gly Gly Cys Ser His Gly Cys Ser His Thr
340 345 350

Ser Thr Gly Pro Leu Cys Thr Cys Pro Arg Gly Tyr Glu Leu Asp Glu
355 360 365

Asp Gln Lys Thr Cys Ile Asp Ile Asp Asp Cys Ala Asn Ser Pro Cys
370 375 380

Cys Gln Gln Ala Cys Ala Asn Thr Pro Gly Gly Tyr Glu Cys Ser Cys
385 390 395 400

Phe Ala Gly Tyr Arg Leu Asn Thr Asp Gly Cys Gly Cys Glu Asp Val
405 410 415

Asp	Glu	Cys	Ala	Ser	Gly	His	Gly	Gly	Cys	Glu	His	His	Cys	Ser	Asn
			420				425						430		
Leu	Ala	Gly	Ser	Phe	Gln	Cys	Phe	Cys	Glu	Ala	Gly	Tyr	Arg	Leu	Asp
			435				440					445			
Glu	Asp	Arg	Arg	Gly	Cys	Thr	Ser	Leu	Glu	Glu	Ser	Val	Val	Asp	Leu
			450			455					460				
Asp	Gly	Arg	Leu	Pro	Phe	Val	Arg	Pro	Leu	Pro	His	Ile	Ala	Val	Leu
			465			470				475			480		
Arg	Asp	Glu	Leu	Pro	Arg	Leu	Phe	Gln	Asp	Asp	Tyr	Gly	Ala	Glu	Glu
			485			490					495				
Glu	Ala	Ala	Ala	Ala	Glu	Leu	Arg	Gly	Glu	His	Thr	Leu	Thr	Glu	Lys
			500				505					510			
Phe	Val	Cys	Leu	Asp	His	Ser	Phe	Gly	His	Asp	Cys	Ser	Leu	Thr	Cys
			515			520				525					
Asp	Asp	Cys	Arg	Asn	Gly	Gly	Thr	Cys	Phe	Pro	Gly	Gln	Asp	Gly	Cys
			530			535				540					
Asp	Cys	Pro	Glu	Gly	Trp	Thr	Gly	Ile	Ile	Cys	Asn	Glu	Thr	Cys	Pro
			545			550				555			560		
Pro	Asp	Thr	Phe	Gly	Lys	Asn	Cys	Ser	Ser	Pro	Cys	Thr	Cys	Gln	Asn
			565			570				575					
Gly	Gly	Thr	Cys	Asp	Pro	Val	Leu	Gly	Ala	Cys	Arg	Cys	Pro	Pro	Gly
			580			585				590					
Val	Ser	Gly	Ala	His	Cys	Glu	Asp	Gly	Cys	Pro	Lys	Gly	Phe	Tyr	Gly
			595			600				605					
Lys	His	Cys	Arg	Lys	Lys	Cys	His	Cys	Ala	Asn	Arg	Gly	Arg	Cys	His
			610			615				620					
Arg	Leu	Tyr	Gly	Ala	Cys	Leu	Cys	Asp	Pro	Gly	Leu	Tyr	Gly	Arg	Phe
			625			630			635			640			
Cys	His	Leu	Ala	Cys	Pro	Pro	Trp	Ala	Phe	Gly	Pro	Gly	Cys	Ser	Glu
			645			650				655					
Asp	Cys	Leu	Cys	Glu	Gln	Ser	His	Thr	Arg	Ser	Cys	Asn	Pro	Lys	Asp
			660			665				670					

Gly Ser Cys Ser Cys Lys Ala Gly Phe Gln Gly Glu Arg Cys Gln Ala
675 680 685

Glu Cys Glu Ser Gly Phe Phe Gly Pro Gly Cys Arg His Arg Cys Thr
690 695 700

Cys Gln Pro Gly Val Ala Cys Asp Pro Val Ser Gly Glu Cys Arg Thr
705 710 715 720

Gln Cys Pro Pro Gly Tyr Gln Gly Glu Asp Cys Gly Gln Glu Cys Pro
725 730 735

Val Gly Thr Phe Gly Val Asn Cys Ser Gly Ser Cys Ser Cys Val Gly
740 745 750

Ala Pro Cys His Arg Val Thr Gly Glu Cys Leu Cys Pro Pro Gly Lys
755 760 765

Thr Gly Glu Asp Cys Gly Ala Asp Cys Pro Glu Gly Arg Trp Gly Leu
770 775 780

Gly Cys Gln Glu Ile Cys Pro Ala Cys Glu His Gly Ala Ser Cys Asn
785 790 795 800

Pro Glu Thr Gly Thr Cys Leu Cys Leu Pro Gly Phe Val Gly Ser Arg
805 810 815

Cys Gln Asp Thr Cys Ser Ala Gly Trp Tyr Gly Thr Gly Cys Gln Ile
820 825 830

Arg Cys Ala Cys Ala Asn Asp Gly His Cys Asp Pro Thr Thr Gly Arg
835 840 845

Cys Ser Cys Ala Pro Gly Trp Thr Gly Leu Ser Cys Gln Arg Ala Cys
850 855 860

Asp Ser Gly His Trp Gly Pro Asp Cys Ile His Pro Cys Asn Cys Ser
865 870 875 880

Ala Gly His Gly Asn Cys Asp Ala Val Ser Gly Leu Cys Leu Cys Glu
885 890 895

Ala Gly Tyr Glu Gly Pro Arg Cys Glu Gln Ser Cys Arg Gln Gly Tyr
900 905 910

Tyr Gly Pro Ser Cys Glu Gln Lys Cys Arg Cys Glu His Gly Ala Ala
915 920 925

Cys Asp His Val Ser Gly Ala Cys Thr Cys Pro Ala Gly Trp Arg Gly
930 935 940

Ser Phe Cys Glu His Ala Cys Pro Ala Gly Phe Phe Gly Leu Asp Cys
945 950 955 960

Asp Ser Ala Cys Asn Cys Ser Ala Gly Ala Pro Cys Asp Ala Val Thr
965 970 975

Gly Ser Cys Ile Cys Pro Ala Gly Arg Trp Gly Pro Arg Cys Ala Gln
980 985 990

Ser Cys Pro Pro Leu Thr Phe Gly Leu Asn Cys Ser Gln Ile Cys Thr
995 1000 1005

Cys Phe Asn Gly Ala Ser Cys Asp Ser Val Thr Gly Gln Cys His Cys
1010 1015 1020

Ala Pro Gly Trp Met Gly Pro Thr Cys Leu Gln Ala Cys Pro Pro Gly
1025 1030 1035 1040

Leu Tyr Gly Lys Asn Cys Gln His Ser Cys Leu Cys Arg Asn Gly Gly
1045 1050 1055

Arg Cys Asp Pro Ile Leu Gly Gln Cys Thr Cys Pro Glu Gly Trp Thr
1060 1065 1070

Gly Leu Ala Cys Glu Asn Glu Cys Leu Pro Gly His Tyr Ala Ala Gly
1075 1080 1085

Cys Gln Leu Asn Cys Ser Cys Leu His Gly Gly Ile Cys Asp Arg Leu
1090 1095 1100

Thr Gly His Cys Leu Cys Pro Ala Gly Trp Thr Gly Asp Lys Cys Gln
1105 1110 1115 1120

Ser Ser Cys Val Ser Gly Thr Phe Gly Val His Cys Glu Glu His Cys
1125 1130 1135

Ala Cys Arg Lys Gly Ala Ser Cys His His Val Thr Gly Ala Cys Phe
1140 1145 1150

Cys Pro Pro Gly Trp Arg Gly Pro His Cys Glu Gln Ala Cys Pro Arg
1155 1160 1165

Gly Trp Phe Gly Glu Ala Cys Ala Gln Arg Cys Leu Cys Pro Thr Asn
1170 1175 1180

Ala Ser Cys His His Val Thr Gly Glu Cys Arg Cys Pro Pro Gly Phe
1185 1190 1195 1200

Thr Gly Leu Ser Cys Glu Gln Ala Cys Gln Pro Gly Thr Phe Gly Lys
1205 1210 1215

Asp Cys Glu His Leu Cys Gln Cys Pro Gly Glu Thr Trp Ala Cys Asp
1220 1225 1230

Pro Ala Ser Gly Val Cys Thr Cys Ala Ala Gly Tyr His Gly Thr Gly
1235 1240 1245

Cys Leu Gln Arg Cys Pro Ser Gly Arg Tyr Gly Pro Gly Cys Glu His
1250 1255 1260

Ile Cys Lys Cys Leu Asn Gly Gly Thr Cys Asp Pro Ala Thr Gly Ala
1265 1270 1275 1280

Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp Cys Ser Leu Ala Cys
1285 1290 1295

Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His Val Cys Ala Cys Arg
1300 1305 1310

Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Ala Cys Ile Cys Ser Pro
1315 1320 1325

Gly Lys Thr Gly Val Arg Cys Glu His Gly Cys Pro Gln Asp Arg Phe
1330 1335 1340

Gly Lys Gly Cys Glu Leu Lys Cys Ala Cys Arg Asn Gly Gly Leu Cys
1345 1350 1355 1360

His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met Gly Pro
1365 1370 1375

His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala Cys Leu
1380 1385 1390

Leu Glu Cys Phe Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr Thr Gly
1395 1400 1405

Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu His Ser
1410 1415 1420

Cys Pro Ser Gly Phe His Gly Pro Gly Cys Gln Arg Val Cys Glu Cys
1425 1430 1435 1440

Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Gln Cys Leu Cys Pro
 1445 1450 1455

 Ala Gly Phe His Gly Gln Phe Cys Glu Lys Gly Cys Glu Ser Gly Ser
 1460 1465 1470

 Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys His Thr Gly Val Pro
 1475 1480 1485

 Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg Thr Gly
 1490 1495 1500

 Ala Ala Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro Gly Cys
 1505 1510 1515 1520

 Ala Leu Arg Cys Asp Cys Gly Gly Ala Asp Cys Asp Pro Ile Ser
 1525 1530 1535

 Gly Gln Cys His Cys Val Asp Ser Tyr Met Gly Pro Thr Cys Arg Glu
 1540 1545 1550

 Val Pro Thr Gln Ile Ser Ser Arg Pro Ala Pro Gln His Pro Ser
 1555 1560 1565

 Ser Arg Ala Met Lys His
 1570

<210> 78
 <211> 1708
 <212> DNA
 <213> Homo sapiens

<400> 78
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 cgccggcgcg tccccccagtc tggtggccga gctgcagggc gcccctggacg cctgcgcaca 180
 ggcacaattt caattggagc agagcctgcg cgtttgcgtt cggctgtgc atgcctggaa 240
 accaactggg accccgggctt tgaagccacc tccaggggcca gaaactaatg gagaggaccc 300
 cttccagca tgcacaccca gtcacacaaga cctcaaagag ttggagtttc tgacccagggc 360
 actggagaag gctgtacgag ttcaagagg catcactaag gccggagaga gagacaaggc 420
 ccccaagcctg aaatcttagt ccattgtcac ctcttctggc acgacagcct ccgcggccacc 480
 gcatctccca ggccaagctg gtggccatgc ttcaagacacg agacccacca agggcctccg 540
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 gacccgtttt gggatggag cccgaacccc caggcctggg gcgggcctca gggaccagca 660
 aatggcccca tccgctgctc ctcaggcccc agaagccttc acactcaagg agaaggggca 720
 cctgctgccc ctgcctgccc cattcaggaa agcagcttcc cagaactcga gcctgtgggc 780
 ccagctcagt tccacacaga ccagtgattt cacggatgcc gccgctgcca aaacccagtt 840

cctccagaac atgcagacag cttcaggcg gccccagccc aggctcatg ctgtggaggt 900
 ggaggcggag gcggggcgcc tgcggaaggc ctgctcgctg ctgagactgc gcatgaggga 960
 ggagctctca gcagcccca tggactggat gcaggagtac cgctgcctgc tcacgctgga 1020
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 ggccgaacag ccaccaagac catgtcctgt ggggaggccc cccggagcct cgccgtcctg 1140
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 ttcagatggg gattgggggt gtctccctg gcactgtgct cggggaccca gagatgcctg 1500
 tgcttccctg gaaaacctgg tgaactggac caggtggcct cactggctt tctcaggaca 1560
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 gtgtgatatt aaagccactt tagaaagc 1708

<210> 79

<211> 1151

<212> PRT

<213> Gallus gallus

<400> 79

Arg Ser Pro Thr Pro Pro Arg Asn Pro Pro Pro Thr Pro Pro Pro Ala

1

5

10

15

Pro Ser Pro Ala Pro Ala Pro Ala Pro Ala Pro Thr Ala Pro Pro Arg

20

25

30

Pro Lys Trp Val Pro Ile Ala Glu Leu His Pro Ala Ala Pro Gln Pro

35

40

45

Pro Pro Lys Trp Val Pro Ile Gly Gly Ala Pro Pro Pro Pro Gly Thr

50

55

60

Glu Pro Thr Pro Pro Ser Lys Pro Thr Asp Gly Ala Asp Ala Ala Pro

65

70

75

80

Lys Ala Ser Ala Glu Leu Thr Ser Pro Pro Pro Ala Ser Pro Ser Pro

85

90

95

Pro Asp Gly Pro Lys Ala Pro Ser Gly Ala Gly Glu Ala Glu Ala Gly

100

105

110

Thr Pro Pro Pro Ser Gln Gly Pro Ala Gly Thr Pro Pro Pro Ser Gln

115

120

125

Gly Ala Ala Gly Ala Pro Lys Gly Asp Gly Thr Ala Gln Pro Ser Gly

130	135	140
Thr Lys Ser Gly Ala Asp Gly Lys Pro Ala Ala Gln Asp Val Pro Lys		
145	150	155
Ala Thr Thr Ala Ala Thr Glu Ala Arg Pro Ala Ser Ala Ala Ser Pro		
165	170	175
Thr Val Pro Lys Ala Thr Ala Glu Ala Thr Ala Val Thr Ala Ala Ser		
180	185	190
Gln Ser Ala Pro Lys Ala Ala Thr Asp Ala Ala Ala Val Thr Ala Ala		
195	200	205
Ser Gln Ser Ala Pro Lys Ala Thr Val Glu Val Lys Pro Ala Ala Ala		
210	215	220
Ala Val Ala Lys Glu Ala Lys Ala Val Thr Ala Ala Ala Ala Pro		
225	230	235
Lys Ala Thr Ala Glu Ala Lys Pro Ala Pro Val Thr Ser Pro Thr Ile		
245	250	255
Pro Cys Ser Ser Ala Glu Ala Lys Pro Leu Thr Ala Ala Ser Pro Thr		
260	265	270
Ala Ser Lys Ala Thr Ala Glu Ala Lys Pro Val Pro Ala Thr Ala Ser		
275	280	285
Leu Met Ala Thr Lys Val Thr Ala Glu Ala Lys Pro Ala Pro Ser Pro		
290	295	300
Ser Val Pro Lys Ala Thr Thr Asp Thr Lys Ala Val Thr Ala Thr Ala		
305	310	315
Pro Lys Ala Gly Pro Asp Val Lys Pro Ala Val Ala Val Cys Ala Glu		
325	330	335
Ala Lys Pro Ala Pro Pro Pro Pro Gln Gln Leu Pro Lys Ala Ala		
340	345	350
Ala Ala Ala Ala Pro Thr Gly Thr Glu Leu Lys Pro Ala Thr Ala Pro		
355	360	365
Pro His Gly Ser Pro Arg Ala Asn Ser His Thr Val Thr Val Thr Pro		
370	375	380
Pro Asn Val Pro Arg Ala Ala Ala Thr Val Pro Thr Ala Gly Ala		

385	390	395	400
Val Pro Lys Ala Ser Thr Gly Thr Thr Pro Ala Ala Ala Pro Gln Gln			
405	410	415	
Pro Val Pro Lys Ala Ala Pro Val Thr Pro Pro Ser Pro Gln Gln Ala			
420	425	430	
Val Pro Arg Ala Ala Thr Ala Ala Ala Pro Val Thr Pro Gln Gln			
435	440	445	
Pro Val Thr Lys Ala Ala Thr Thr Thr Asn Ala Thr Pro Pro Pro Gln			
450	455	460	
Pro Ile Pro Lys Ala Ala Thr Thr Thr Ala Thr Pro Val Thr Pro			
465	470	475	480
Gln Gln Pro Ile Pro Lys Ala Gly Thr Asp Ala Ala Pro Pro Pro Ala			
485	490	495	
Val Pro Lys Ala Pro Ser Asp Gly Arg Ala Ala Thr Pro Gly Val Pro			
500	505	510	
Asn Ala Ala Thr Asp Pro Gln Lys Pro Pro Pro Thr Pro Gln Ser Val			
515	520	525	
Pro Ser Ala Val Thr Glu Pro Lys Pro Gln Pro Arg Ala Ala Pro Pro			
530	535	540	
Pro Ser Asn Glu Ala Thr Pro Ala Val Pro Ser Pro Ser Pro Asn Leu			
545	550	555	560
Lys Ser Pro Leu Pro Thr Ile Pro Lys Pro Val Pro Leu Met Ala Leu			
565	570	575	
Thr Pro Gln Pro Val Thr Ala Gln Met Val Thr Gln Leu Ala Ala Thr			
580	585	590	
Lys Pro Ser Pro Ile Val Pro Lys Ala Ser Pro Lys Ala Leu Met Thr			
595	600	605	
Pro Pro Pro Pro Pro Gly Leu Pro Arg Ala Leu Ala Ala Ala Lys			
610	615	620	
Leu Leu Gly Leu Pro Ser Ser Pro Val Ala Ser Ala Met His Ala Lys			
625	630	635	640
Val Thr Pro Arg Pro Leu Pro Ala Ser Pro Val Pro Met Ala Ala Ser			

645	650	655
Pro Ala Ser Leu Gly Pro Asp Ala Ala Arg Val Ala Leu Ala Thr Asn		
660	665	670
Ala Ala Ser Pro Gly Ala Lys Pro Glu Ala Ala Gly Gly Asn Gly Thr		
675	680	685
Leu Met Ala Pro Met Gly Ala Ala Asn Thr Gln Met Ala Pro Ile Gly		
690	695	700
Ala Ala Gly Ala Ala Gln Thr Ala Pro Met Gly Ala Ala His Thr His		
705	710	715
Val Ser Pro Met Gly Ala Gly Gly Ala Thr Gln Met Ser Pro Thr Gly		
725	730	735
Ala Ala Asn Thr His Met Ser Pro Ile Gly Ala Gly Gly Ala Thr Gln		
740	745	750
Met Ser Pro Met Gly Ala Ala Asn Thr Gln Met Ser Pro Met Gly Ala		
755	760	765
Thr Thr Thr Gln Met Ser Pro Met Gly Ala Ala Ala Thr Thr Gln Pro		
770	775	780
Ser Pro Met Gly Ala Ala Ala Thr Gln Val Thr Ala Thr Ser Ala Gly		
785	790	795
Asn Thr Met Gln Val Ser Pro Met Gly Ala Ala Thr Pro Pro Gln Thr		
805	810	815
Pro Ser Val Gly Ala Ala Thr Thr Pro Gln Pro Ser Pro Met Gly Ala		
820	825	830
Ala Thr Thr Leu Met Ser Pro Met Gly Ala Ala Thr Thr Pro Gln Pro		
835	840	845
Ser Pro Met Gly Ala Val Thr Thr Gln Pro Pro Pro Met Ala Ala Thr		
850	855	860
Asn Thr Thr Gln Pro Pro Pro Met Ala Ala Ser Thr Pro Gln Ser Thr		
865	870	875
Pro Met Gly Ala Ala Thr Thr Gln Ser Pro Pro Met Gly Ala Thr		
885	890	895
Thr Thr Gln Ser Pro Pro Met Gly Ala Ser Thr Pro Gln Ala Pro Pro		

900	905	910
Thr Val Ala Gly Ser Pro Thr Pro Pro Pro Pro Ile Pro Pro Ser Pro		
915	920	925
Thr Ala Gln Thr Ser Pro Gln Pro Met Ser Lys Ser Pro Pro Pro Asp		
930	935	940
Pro Pro Lys Ala Pro Ser Ala Ala Gln Thr Ser Pro Ala Ala His		
945	950	955
Val Ala Asn Ala Ser Pro Gly Val Thr Ala Val Ser Pro Ala Pro Ile		
965	970	975
Gly Val Thr Glu Ala Ser Pro Ser Ala Asp Gly Ala Arg Leu Ser Pro		
980	985	990
Gly Pro Thr Ala Ala Thr Asp Gly Pro Lys Ala Ser Pro Ala Ala Thr		
995	1000	1005
Ala Asp Val Thr Glu Ala Ala Thr Asp Val Thr Ala Ala Ala Thr Ala		
1010	1015	1020
Val Pro Ala Glu Ala Ala Pro Thr Lys Ala Lys Arg Ser Ser Ser Ser		
1025	1030	1035
1040		
Ser		
1045	1050	1055
Ser Ser Ser Ser Asp Ser Asp Ser Ser Ser Ser Ser Ser Glu Ser Asn		
1060	1065	1070
Pro Ala Ser Pro Ala Pro Ala Val Gly Asp Gly Gln Gln Gln Met Thr		
1075	1080	1085
Pro Gly Ala Ala Gln Ser Val Pro Pro Val Thr Glu Ala Ala Val Gln		
1090	1095	1100
Glu Ala Ala Ala Ala Ala Ala Ala Gly Ala Glu Arg Glu Gly		
1105	1110	1115
1120		
Arg Pro Thr Arg Arg Lys Lys Arg Thr Arg Ser Ser Ser Ser Ser		
1125	1130	1135
Ser		
1140	1145	1150

<210> 80
<211> 199
<212> PRT
<213> Homo sapiens

<400> 80
Met Asn Cys Val Cys Arg Leu Val Leu Val Val Leu Ser Leu Trp Pro
1 5 10 15

Asp Thr Ala Val Ala Pro Gly Pro Pro Pro Gly Pro Pro Arg Val Ser
20 25 30

Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr Arg Ser
35 40 45

Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe
50 55 60

Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu Ala Met
65 70 75 80

Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu Thr Arg
85 90 95

Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp Leu Arg
100 105 110

Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr
115 120 125

Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu Leu Met
130 135 140

Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro
145 150 155 160

Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala His Ala
165 170 175

Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg Gly Leu
180 185 190

Leu Leu Leu Lys Thr Arg Leu
195

<210> 81
<211> 1029

<212> DNA

<213> Homo sapiens

<400> 81

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ccctccctgt cagggcgtaa ttgagtcaaa ggcaggatca ggttccccgc cttccagtcc 180
aaaaatcccg ccaagagagc cccagagcag agaaaaatcc aaagtggaga gaggggaaga 240
aagagaccag tgagtcatcc gtccagaagg cggggagagc agcagcggcc caagcaggag 300
ctgcagcagc cgggtacact ggactcagcg gtagcaacct cgccccctgc aacaaaggca 360
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agcgtcgaaa atttgagct gccttctgg cattcatttt catactggca gctgtggata 480
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aatggcagtg gagttgtgtgt gtgcccacca gtggagactg tggctggc acacgggagg 600
gcactcggac tggagctgag tgcaagcaaa ccatgaagac ccagagatgt aagatcccct 660
gcaactggaa gaagaattt ggcgcggagt gcaaatacca gttccaggcc tggggagaat 720
gtgacctgaa cacagccctg aagaccagaa ctgaaagtct gaagcggcc ctgcacaatg 780
ccgaatgcca gaagactgtc accatctcca agccctgtgg caaactgacc aagcccaaac 840
ctcaaggcaga atctaagaag aagaaaaagg aaggcaagaa acaggagaag atgctggatt 900
aaaagatgtc acctgtggaa cataaaaaagg acatcagcaa acaggatcag ttaactattg 960
catttatatg taccgttaggc tttgtattca aaaattatct atagctaagt acacaataag 1020
caaaaacaa 1029

<210> 82

<211> 216

<212> PRT

<213> Homo sapiens

<400> 82

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 83

<211> 346

<212> PRT

<213> Rattus norvegicus

<400> 83

Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
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Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn
20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu
35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys
50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp
65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala
85 90 95

Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His Tyr
100 105 110

Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala Met
115 120 125

Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser Ser
130 135 140

Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp Ala
145 150 155 160

Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr Tyr Gln Arg Leu Phe
165 170 175

His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu His Trp Pro Asn Gln
180 185 190

Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr Leu
195 200 205

Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn His
210 215 220

Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser Lys
225 230 235 240

Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Phe Gly Ile
245 250 255

Ser Trp Leu Pro His His Val Ile His Leu Trp Ala Glu Phe Gly Ala
260 265 270

Phe Pro Leu Thr Pro Ala Ser Phe Phe Arg Ile Thr Ala His Cys
275 280 285

Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe Leu
290 295 300

Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys Arg Val
305 310 315 320

Cys Asn Glu Ser Pro His Gly Asp Ala Lys Glu Lys Asn Arg Ile Asp
325 330 335

Thr Pro Pro Ser Thr Asn Cys Thr His Val
340 345

<210> 84
<211> 1308
<212> DNA
<213> Bos taurus

<400> 84
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ccgaggccgc aggaggagcc ccagc当地 c当地 ccccacagc agc当地 gaagc tc当地 ggagcc 180
ccc当地 gaggg gccc当地 c当地 tt当地 acgatgc当地 gagt当地 acatgc当地 tgtcaatcta caggacttac 240
tccatcgccg agaagctggg catcaatgct agcttttcc agtcttccaa gtc当地 ggctaa 300
acgatcacta gctt当地 ttaga cagggacta gacgatctc cgc当地 acactcc tctccggaga 360
cagaagtatt tggtt当地 ttagt gtccacgctc tc当地 agacaag aagagctggt gggc当地 gggac 420
gtgc当地 ggctgt ttc当地 gccaggc gccc当地 ctggcc当地 cggc当地 gggccgc tccgcttgca 480
gctctt当地 ccc tgc当地 cagtc当地 cc当地 ctgctgct ggaagc当地 cgg agc当地 ctggacc cgc当地 agggccg 540
cccc当地 ggccgc gctgggaagt cttc当地 gagctg tggc当地 gggcc tgc当地 cccca gc当地 cctt当地 ggaag 600
cagctgtgct tggagcttc当地 ggccgctgg ggccglocal gacgc cggc当地 gggccgc ggaggacgag 660
gc当地 cgc当地 acgc c当地 tggccccc当地 gc当地 agccggccg cccccc当地 ggacc tgc当地 ggagtct ggctt当地 cggc 720
cggagggtgc ggacccccc当地 ggagc当地 ggc当地 tt当地 gctctgctg tgc当地 tt当地 cc当地 agtgc当地 780
aagaccctgt tc当地 gccgagat ggc当地 gagc当地 ctgggctc当地 cgaccgaggt gtc当地 ggcccc 840
ggtggtgggg cc当地 gagggggtc gggccgccc当地 cc当地 gccc当地 cccgccc当地 ggc当地 ctggggcc 900
acccc当地 ggacg ctgggctctg gtc当地 gccc当地 cctggccggc ggc当地 ggccgc当地 acg ggctt当地 cggc 960
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<211> 436
<212> PRT
<213> Bos taurus

<400> 85
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1 5 10 15

Glu Gly Arg Met Pro Arg Ala Pro Arg Glu Asn Ala Thr Ala Arg Glu
20 25 30

Pro Leu Asp Arg Gln Glu Pro Pro Pro Arg Pro Gln Glu Glu Pro Gln
35 40 45

Arg Arg Pro Pro Gln Gln Pro Glu Ala Arg Glu Pro Pro Gly Arg Gly

50	55	60
Pro Arg Leu Val Pro His Glu Tyr Met Leu Ser Ile Tyr Arg Thr Tyr		
65	70	75
Ser Ile Ala Glu Lys Leu Gly Ile Asn Ala Ser Phe Phe Gln Ser Ser		
85	90	95
Lys Ser Ala Asn Thr Ile Thr Ser Phe Val Asp Arg Gly Leu Asp Asp		
100	105	110
Leu Ser His Thr Pro Leu Arg Arg Gln Lys Tyr Leu Phe Asp Val Ser		
115	120	125
Thr Leu Ser Asp Lys Glu Glu Leu Val Gly Ala Asp Val Arg Leu Phe		
130	135	140
Arg Gln Ala Pro Ala Ala Leu Ala Pro Pro Ala Ala Pro Leu Ala		
145	150	155
Ala Leu Arg Leu Pro Val Ala Pro Ala Ala Gly Ser Ala Glu Pro Gly		
165	170	175
Pro Ala Gly Ala Pro Arg Pro Gly Trp Glu Val Phe Asp Val Trp Arg		
180	185	190
Gly Leu Arg Pro Gln Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala		
195	200	205
Ala Trp Gly Gly Glu Pro Gly Ala Ala Glu Asp Glu Ala Arg Thr Pro		
210	215	220
Gly Pro Gln Gln Pro Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly		
225	230	235
Arg Arg Val Arg Thr Pro Gln Glu Arg Ala Leu Leu Val Val Phe Ser		
245	250	255
Arg Ser Gln Arg Lys Thr Leu Phe Ala Glu Met Arg Glu Gln Leu Gly		
260	265	270
Ser Ala Thr Glu Val Val Gly Pro Gly Gly Ala Glu Gly Ser Gly		
275	280	285
Pro Pro Pro Pro Pro Pro Pro Pro Ser Gly Thr Pro Asp Ala		
290	295	300
Gly Leu Trp Ser Pro Ser Pro Gly Arg Arg Arg Arg Thr Ala Phe Ala		

305	310	315	320
Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu Arg Cys Ser			
325	330	335	
Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp Asp Trp			
340	345	350	
Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Val Cys			
355	360	365	
Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Ile Ile			
370	375	380	
Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro Ser Cys			
385	390	395	400
Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile Asp Ala			
405	410	415	
Gly Asn Asn Val Val Tyr Asn Glu Tyr Glu Glu Met Val Val Glu Ser			
420	425	430	
Cys Gly Cys Arg			
435			